>SGPR397_SEQID_1

ATTGGTCCTGCCTTTTGTCAGTGGTTTGTAAAAGAAGCTCTTCTAACATATAAGAGTGACCCAGCCATGAGAAAA TGCTGAATCATCTATATTTCTATATCATGCCTGTGTTTAACGTCGATGGATACCATTTTAGTTGGACCAATGATCGA AGAGGAAGCATATGCACTGAAGAAAATATCCTATCAACTTAAGGTGGACCTGTGGCAGCCCAGCAGTATCTCCTA ATTTTAAAGCTGGGCAGACGATCACGACTCAAAAGAGCTGTTTGGATAGACTGTGGGTATTCATGCAAGAGAATGG GCAACCGGGGCACAGCCACCTTTATAACAACCGCTATGCTGGTGATAAAGTGATAAGATTTATTCCCAAAACAGA TGTATCAGAGGGAACAGTTACTGATGTCCATATCCCCCAAAATGGTTCCCGAGCCCTGTTAGCCTTCTTACAGGA AGCCAACATCCAGTACAAGGTCCTCATAGAAGATCTTCAGAAAACACTGGAGAAGGGAAGCAGCTTGCACACCC AGAGAAACCGAAGATCCCTCTGGATATAATTATGAAGTTTATCACTCCTTAGAAGAAATTCAAAATTGGATGCA GAAGTGGTGGTAAGTTTGGGACCAACTGGGATCCAGATCCAAAGGTTTCTGCAGGTTTTACTCTGCAAATAT TTTGGAGAAAAACAAGGTCAAGGAACTCAAGGTTTCGCTGCCGTGGAGTGGATGCCAATAGAAACTGGAAAGT ATGAAGTGTCTCGGGAAGCGCAGGGGCCAGGCAGCTGCTTTCCTGCCTCTTTGCTGGCTCTTTTGAAGATTCT ICATCTGAATAAAACTCACTCAGGCCTCATTCACATGTTCTCTATTGGAAGATCATATGAGGGAAGATGTCTTTT GAGTCCAGAGGACTCTCATGGGAGACTCATGTTTTCTGTATGTGA

>SGPR413 SEQID 2

FIG. 1A

CATGTTTTGGGACGGATCTCAATCGAATTTCAATGCATCTTGGTGTAGTATTGGTGCCTCTAGAAACTGCCAAGA GCCCAACACAGAGAGAGATTGTGGACAAGTCAGTGAGTCCATGGAGCCTGGAGACGTATTCCTATAACATATAC AACATAGATGGTTATATCTACACTTGGACAACTGATCGTCTTTGGAGGAAATCCCGTTCACCCCATAATAATGGCA <u> CCAGCCCACCTGTGAGGAGCCATGGAGGCTGTGCTGTCAGTCCTGGATGATGTGTATGCGAAACACTGGCACT</u> 4 GGATGATATTTTGTGCTTCCTGACCATGCACTCTTATGGGCAGTTAATTCTCACACCTTACGGCTACACAAAAA -AAATCAAGTAACCACCCAGAAATGATTCAAGTTGGACAGAAGGCAGCAAATGCATTGAAAGCAAAGTATGGAAC IGGGATTCCCTTCTCATATACGTTTGAGCTGAGGGACAGTGGAACATATGGGTTTGTTCTGCCAGAAGCTCAGAT ATGAAGCCTCTGCTTGAAACCCTTTATCTTTTGGGGATGCTGGTTCCTGGAGGGCTGGGATATGATAGATCCTTA SGGACAGTGCTGGAAGGGTGACATCTGCCACTATGCTGCTGGGCCTGCTGGTGTCCTGCATGTCTTCTTCTAA CCTAGGAGTGACCTATGAGACCCACCCCATGTATTATCTGAAGATCAGCCAACCATCTGGTAATCCCAAGAAAT TCAAACATTCTGTGGGACAGGGCCAGTGTCTGAACCAGAGACTAAAGCTGTTGCCAGCTTCATAGAGAGCAAGA CACCCCATGGGAGAGATCTATGAGTGGATGAGAGAGATCAGTGAGAAGTACAAGGAAGTGGTGACACAGCATTT CATTTGGATGGACTGTGGAATTCACGCCAGAGAATGGATTGCTCCTGCTTTTTGCCAATGGTTCGTCAAAGAAAT CAATTATAGAGTTGGATCGAGTGCAGATATTTTATATGCCTCATCAGGGTCTTCAAGAGATTGGGCCCGAGACAT ICTACAAAACCATAAAGACAACTCAAGTATACGCAAGCTCCTTAGGAACCTGGACTTCTATGTCCTTCCAGTTCT

GTTTCACTGCATCCACCAAGAACTGTATGGTTGGCTATGACATGGGGGCCCACAAGGTGTGACTTCACACTTAGCA AGCTGTATGCTGTGGAGATCTCAGATCACCCTGGGGAGCATGAAGTCGGTGAGCCCGAGTTCCACTACATCGCG GAATTGACATCAACAACAACTTTCCTGATTTAAACACGCTGCTCTGGGAGGCAGAGGATCGACAGAATGTCCCCA ACGGAGGACTTCCAGAAGGAGGAGGGCACTGTCAATGGGGCCTCCTGGCACACCGTCGCTGGAAGTCTGAACG ATCACCGCCGGAACGAGATGACCACCACTGATGACCTGGATTTTAAGCACCACAATTATAAGGAAATGCGCCAGI ATGECTACGAGAGGCCTACGAAGGGGGCTCGGAGCTGGGAGGCTGGTCCCTGGGACGCTGGACCCACGATG AGAGCAGTCATAGCCTGGATGGAAAAAATCCCTTTTGTGCTGGGCGGCAACCTGCAGGGCGGCGGCGGTGGTGG TGGCGTACCCCTACGACCTGGTGCGGTCCCCCTGGAAGACGCAGGAACACACCCCCCACCCCCGACGACCACG <u>AGCTGCCCGAGGAGTGGGAGAATAACCGGGAATCTCTGATCGTGTTCATGGAGCAGGTTCATGGTGGCATTAAA</u> GGCTTGGTGAGAGATTCACATGGAAAAGGAATCCCAAACGCCATTATCTCCGTAGAAGGCATTAACCATGACATC GTTCCGCTGGCTGGCCTACTCCTATGCCTCCACACACGCCTCATGACAGACGCCCGGAGGAGGGTGTGCCAC CGAACAGCCAACGATGGGGGATTACTGGCGCCTCCTGAACCCTGGAGAGTATGTGGTCACAGCAAAGGCCGAAG CCTGGTTTGATAATGGGAGCATCTGCATGAGAATGGAGATCCTGGGCTGCCCACTGCCAGATCCTAATAATTATT TGATGAAAGTTGTGAATGAAATGTGTCCCAATATCACCAGAATTTACAACATTGGAAAAAGCCACCAGGGCCTGA ATGGTGAGCAATGACAGCCACACGTGGGTCACTGTTAAGAATGGATCTGGAGACATGATATTTGAGGGAAACAG GGGCCCACGCCAATGAGGTGCTGGGCCGGGAGCTGCTGCTGCTGCTGGTGCAGTTCGTGTGTCAGGAGTAC GGAAAGTTCCCAATCACTATATTGCAATCCCTGAGTGGTTTCTGTCGGAAAATGCCACGGTGGCTGCCGAGACC ATTICAGCTACCTTCATACAAACTGCTTCGAACTGTCCATCTACGTGGGCTGTGATAAATACCCACATGAGAGCC TGAGAAGGAGATCCCTGTTCTCAATGAGCTACCCGTCCCCATGGTGGCCCGCTACATCCGCATAAACCCTCAGT GCTGAAGCTGCGGGGGCGGAAGAGACGACAGCGTGGGTGA

>SGPR536 1 SEQID 4

GTGACCTCTTCTGCAACCGCACGGTCTCCGACTGCTGCCTGACTTCTGGGACTTCTGCCTCGGCGTGCCACCC CAGGAGCAGGACCTGTGCTGCCGCGGCCGTGCCGACGACTGTGCCCTGCCCTACCTGGGCGCCCATCTGTTACT GTCGTGGGCGCCGGGAGCTAGCACCGGGTCTGCACCTGCGGGGCATCCGGGACGCGGGAGGCCGGTACTGC AACCGTTGCACCTGCCAGGAGAACAGGCAGTGGCAGTGTGACCAAGAACCATGCCTGGTGGATCCAGACATGA TCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGGGAACCACAGCGCCTTCTGGGGCATGACCCTGGA I.

CCTTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGGTCG AGAGATACCGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGGGAGAGGAGACGCTGCCAGATGGAAG TCTACCGCCTCGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATG SGGCAAGCGCCAGGCCACTGCCCCACTGCCCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTG GAGGTGCATGAGGACTTCTTCCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTTGGGAGGCCAG GCGCGCGCGTCAATGAGTGCGACATCGAGAGCTTCGTGCTGGGCGTCTGGGGCCGCGTGGGCATGGAGGACAT GCCGCGGTGGCCGTCTCGATGGTGCCTGGTTCCTGCGTCGCCGAGGGGTGGTGTCTGACCACTGCTACC GCTGAACCCAGGGGAGGTGCTTCCCACAGCCTTCGAGGCCTCTGAGAAGTGGCCCAACCTGATTCATGAGCCT

SGPR414 SEQID 5

FIG. 1C

SACCAAATTTACATATTGAGATTATCAAACAGTGCCAAGTGATTTTTGAATTTTTGGCAGCAGAAGGGCGACTGAG AAGGAATATAAGCATTTGGAGATTTTTAATCAAGTAGTGTGTGCACTTATTAACTTAGTGATTGCCCAAGTTCAAGT GCTCAGAAAGGAACATACTCTCAAAATATTTACTTACATCAATTCCTGGACACAGAGGCAATGTCTATGCTGCTTC ATGTGCGAGAACTGCGCAGACCTGGTGGAGGTGTTAAATGAAATATCAGATGTAGAAGGTGGTGATGGACTGCA SCTCCGGGACCAGCTTTGTAAACATTGTACTACCATTAACATAGATTCCACGTGGCAAGATGAGAGAATCAAGC AACTCTACAAGAATTTGTAATCTGACTGAGGAGGAATCTTCAAAGAGTTCTGATCCTTTTAGTTTATGGAGTACAG ATGAGAAGGAAAAACTCTTACTATGTGGGAAAAATTTTTCAAATTCAGTTTCCCTTATATACTGCTTACAAGCAT TGGATACAACATTATGCTTTGATAAAGAAAGCCTAGATCTTGCATTTAAGTACTTTATGTCACCTACTTTGACTATG CGGACACAGAAACGTCCATTGCAAAAGAACTTGCAGACTGGCTTATTAGCAACAATGTGGGGGGGATATATTTG FACTCAACATATTGACTGTATTTGGGCTGCAGCACAGTTGAAACATTGTAGTCGGTATATACATGACTTATTTCCTT CTTTGAATATGGAACTCCTGAAACTTTGCCATTTCTTATAGCACATGCGTTTATTACAGTTGTGTCTAATATTAGAA CTCGGATCAGGAGTTACGACAGAGTGCAGCTCGTAACATGGCTGACTTAATGTGGAGCACAGTCAAAGAACCAT 4GGTTGGCTGGATTGAGTCAGATAACAAATCAACTCCATACCTTCAATGATGTGTGCAATAATGAATCATTAGTAT 'ATGGCTACATATTCCCGCTGTCATGCAGCACATTATACCTTTTAGGACCTATGTTATTAGGTATTTATGCAAGCT

SAGCAAGTTGACATCTTATGGCATTGTTTAGTAGAAGATTCTGAATGTTATGATGATGCACTCCATTGGTTTTAAA GCCTTGAAAACTTGGGAAACAACAGATCAGTAGTAATTTCACTTCGTCTTCCAAAACTATTTGGTACTTTTCAG SCTAAAACCTGAAACAATTAGCATGACTGGCTTAAACCTGTTTCAGCATCTCTGTAACTTGGCTCGATTGGCTACC 4GCAAGAATTTATTAGTAAGTGCATGGAGAGTCTTATGATAGCTTCTAGCAGTCTTGAACAGGAATCACACTCAAG SCTAAGGGTTGTATGCCAGCCAGCTGGACTTCCTGACAAGATGACTATTGAAATGTATCCTAGTGACCAGGTAGC <u> AATCATTGCCATCAGTAGATAATCGAATGCGAATGCTGGATGCTTGTTCACACTCTGAAGACCCAGAACATGATAT</u> CTGGTGATGTCAGTCGAGCAGCTATCCAGTATATTAACTCCTATTATATTAATGGTAAAACAGGTTTGGAGAAGG CAGTAGTGGGCATAGTGATGGATCTAGCAATGAGGTTAATTCTAGCCACGCAAGCCAGTCAGCTGGGAGCCTG CCATCACCACCACCACGATGGGCATATGGTTGATGTATGCTAAGTGCAGATGATGTCAGTTGTAGTAGCTCCCA CTTAGTCAAGGACCTGTAGTTCATAAACATCAATTCAACAGTAATGCTGTTACAGACATTAATTTGGATAATGTTTG CTGAGACAGTGGCAAATTGAAGGCACTGGTATTAGTAGTCATTTGAAAGCACTGAGTGACAAACAGTCTCTGCC CACTCATCAAGAATTTGGATCCCGTACCACTTAGACATCTACTTAATCTGGTCTCAGCTCTTGAGCCAAGTGTTCA CATAATCCTCCCAAAAGCAGTTGTGGTACAGATCTTCGGAATAGAAAGTTAGAGAGTCAAGCAGGCATTTGCCTG TTCAGGGGAAATGAATGCTACTCATATAGCACAAGGGTCTCAGGAGTCTTGTATCACACGAACTGGGGACTTCCT GGTTAGTGCAAAATCAGAAAAAAAAAATATGGCTGATTTTGATGGTGAAGAATCTGGATGTGAAGAGGGGGGCTAGTTCA TCAAGTTCGAAGTAAAGATCAACATGCTATGGGTATGGAAACCTACAAACATCTTTTCCTGGAGAAGATGCCCCA AGTECCTATGATGETTCAAATTCTGAGCTGTGTGTGGACCAATTTTGGGGCATTGCTTTAAGAGCACAA CTCATGGTTATAGAAAGAGGACTCCTTATGCTGAAGACACATCTGGAAGCGTTTAGGAGAAGGTTTGCATATCA TACTGAACAGACACTGTACTTGGCATCCATGTTAATTAAAGCACTGTGGAATAACGCACTAGCAGCTAAGGCTCA TTAGAAGAACAGCTCCATCACCTTGGTCACCTGCAGCTAGTCCTCAAAGCAGTGATAATAGCGATACACATCAAA GTGGAGGTAGTGACATTGAAATGGATGAGCAACTTATTAATAGAACCAAACATGTGCAACAACGACTTTCAGACA GGGGACTCCCAAGGCACGTCAGAAAGAAATGGGACAAGCAGCGGAACAGGAAAGGAACTGGTTTTAACACTG CAGAGGAATCCATGCAGGGAAGTTCTGACGAAACTGCCAACAGTGGTGAAGATGGAAGCAGTGGTCCTGGTAG GCAGTGAGGTACAGTCAGAAGACATTGCAGATATTGAAGCCCTCAAAGAGGAAGATGAAGACGATGATGATGATGTGT TGGGGAGACTATTGGGAATGAATTATTTAATTGTCGACAATTTATTGGTCCACAGCATCACCACCACCACCACCACCACCA GATTAATTCACATGCGGAACTGACATCTCACCTCCAACAACATCTTCCCAATTTAGCTTCCATTTACCATGAACAT CAAGAAAGGAAATACTTTGTTGTGGGATATAGTCCAAGATGAAGATGCAGTTAATCTTTCTGAAGGATTAATAAT GAAGCAGAGAAACTTCTTTGTTCGTTAGTATGTTGGTTTACAGATAGACAAATTCGAATGAGATTCATTGAAGGTT

TTATCCCTGTCAGGGCTGGATGGAGGAGTCCATCAATCGTTCTTTTCTGCTATTGGCTGCCTCAACATTATTGA CAATGTGGCTCTTGGTGAGTTGGGCTCATTGCTGTTCTTTAGTGAAATCTAGCCTTGCTGATAGCGATCATTACA 4GATTGGCTAAAGAAATTGACTCTCCTTATTCCTGAGACTGCAGTTCGTCATGAATCATGCAGTGGTCTCTATAAG AATGTAGAAGATGATGGGCTTACAGGACTCCTAAGGCTTGCAACAAGTGTTGTTAAACACAAACCACCCTTTAAAT AATTTCTTCCTGATGCTCAAGCACTCAAACCTATTAGGATAGATGATTATGAGGAAGAACCAATATTAAAACCAGG TTCAAGGGAAGGACAGGAATTTTTGAGAGATATCTTCAATCTCCTGTTTTTGTTGCCAAGTCTAAAGGACCGACA ICTACTATTCAGCAACTTTATATGATACCTGAGGCAAGACAGGCTGTCTTCACTGCCAAGTATTCAGAGGATATGA 4GCACAAGACCACTCTTCTGGAGCTTCAGAAATGTTTACATATTTAATGGAGAGTGAATGCAAAGCATATAATCC CTCGACTTAGATGCCTTGGCAAGACATTTGGCTGACTGTATTCGAAGTAGGGAGATCCTTGATCATCAGGATGGT STGGCCTCATGAAGATGTCCGTGCTGAATGTAGATTTGTTGGCCTTACTAACCTTGGAGCTACTTGTTACTTAGCT SCCAAGTGGCTGATATGAAGAACATTTATGAATCTCTTGATGAAGTTACTATAAAAGACACTTTGGAAGGTGATAA SATGTATACTTGTTCTCAATGTGGGAAGAAGTACGAGCTGAAAAAAGGGCATGTTTAAGAAATTGCCTCGCATT ACACGAGTTAACAACAGATTATGATGAAAAAGCACTTCATGAGCTTGGTTTTAAGGATATGCAGATGGTATTGTA CATGCAGAAAATCTGTCTAGGCGGGTCTGGGAGCTACTGATGCTTCTTCCTACATGTCCTAATATGTTGATGGCA GAGAACTACAGGCTAATACACACAGGTTATGGCACAACACATGCAGTCCCATGCACGTTATAAATGGGATTA 4GAAGTCAGTGATCATTCAAAAGACTCAGAGAGCTATGAATATGACTTGATAGGAGTGACTGTTCACACAGGAAC CTTTTAATGATGCTGAGGTAAAACCTTTTGATTCTGCTCAACTTGCATCTGAATGTTTTGGTGGAGAGATGATGA GAGTTTGGTCAAAGCAACCGAAAAGGAGAGTTTCCTGGAGGCCTCATGGGACCTGTCAGGATGATTTCATCTGG ACAGCCAAAGTGCAAATCACATTCTTCAAGAGCTGCCGCTTACGATTTGTTAGTAGAGATGGTAAAAGGGGTCTGT TNAGTITCAATACTATGAGATACACATTTAATATGGTCACGATGATGAAAGAGAAAGTGAATACACACTTTTCCTT **3GCAGATGGTGGACACTATTATAGCTTTATCAGAGATATAGTAAATCCCCATGCTTATAAAAACAATAAATGGTAT** ICTTTGGGTGCACCAAGGAGAGAGGGGAAAGGGGGAAGGTGTTCAGCTGCCAGCATCTTGCCTCCCACCCCTC STAATTACAAACAATGTTGTATCCTTGGATTGTGAACATGTTAGTCAAACTGCTGAAGAGTTTTATACTGTGAGGT ITCCAGAATATCTCAGATGAGCAGAGTTTTAAAGCTCAGTCTGATCACAGGTCTAGACATGAAGTTTCACATTATT -AGACCTTTCTGTAAAACATACACCATGGATAAGCAGCCTCTGAATACTGGGGAACAGAAAGATATGACAGAGTT 4GAAGGACAACATTCCAATGCTTTTGCTTTTACAAGAGCCTCATTTAACTACTCTTTTTGATTTATTAGAGATGCT GCATCATTTAAACCACCCTCAGGAAAAGTGGCAGTGGATGATAGTGAGAGCTTACGATGTGAAGAACTTCATCT TTTACTGATCTAATTACCAAAATCGAAGAAATGTCTCCCGAACTGAAAAATACCGTCAAAAGTTTATTTGGAGGT

L

GCTTTGCTCCTGTCAGTACACACTCCCAAACAGTTAAACCCAGCTCTAATTCCAACTCTGCAAGAGCTTTTAAGCA CTCAGTCTGCTATGTCAAAAAACTGCATCAAGCTTTTGTGTGAAGATCCTGTTTTCGCAGAATATATTAAATGTATC CTGGTTCCCTTTCTACAACACAACCATTGTACTTACCATCACAGTAATATACCAATGTCTCTTGGACCTTATTTCCC CTAATGGATGAAAGAACTTTTTAAACAACAACATGTCTACACGTTCATGACACATTTCCTTCTAAAGGTTCAAAG AAGGAGCAACTCCCATTAAAAGGCGGCGTGTTAGCAGTGATGAGGAGCACACTGTAGACAGCTGCATCAGTGAC TATCTCTGCAGTTCTGTCTGACTTAGCTGACTTGAGAAGCTGTGATGGCCAAGCTTTGCCCTCCCAGGACCTGA **GGTTGCTTTATCTCTCAGTTGTGGCCATTCCAGAGGACTCTTTAGTCATATGCAGCAACATGACATTTTAGATACC** ITATCATCAGTTCATCCATCTATTATGCCGAGTTGCAATCAACTGTGAAAAATTTACTGAAACATTAGTTAAGCTGA GTAAAGAATTTAAAGACCTCCACTGTTCCAAGGATTCTACCCTAGCTGAGGAAGAATCTGAGTTCCCTTCTACTTC TGTCGAGAAAATATCAAGCTAATAGGAGGGAAAAGCAATATTCGGCCTCCGCGCCCTGAACTCAATATGTGCCT ICAAGTGTTTTCTGAAGCAAACTGTGCCAATTTGATCAGCACTCTTATTACAAACTTGATAAGCCAGTATCAGAAC CTACAGTCTGATTTCTCCAACCGAGTTGAAATTTCCAAAGCAAGTGCTTCTTTAAATGGGGACCTGAGGGCACTC ATGAAAACAGAAACCAGGGAGGTCCTGACCCCAACGAGCACTTCTGACAATGAGACCAGAGACTCCTCAATTATT GATCCAGGAACTGAGCAAGATCTTCCCTTCCCTGAAAATAGTTCTGTTAAAGAATACCGAATGGAAGTTCCATCT CTGTGTAGGACCATTGAATCTACAATCCATGTCGTCACAAGGATATCTGGCAAAGGAAACCAAGCTGCTTCTTGA CTTGCCCACAATGGTGGAAACCAGTAAGGGCAAAGATGACGTTTATGATCGTATGCTGCTAGACTACTTCTTTTC GTGTCCTAGTTGCCTATGAAGGTTTGCCACTTCATCTTGCACTGTTCCCCCAAACTTTGGACTTGAGGTATGCCAGA CGTTTTCAGAAGACATGTCAAATATCAGGTCACAGCATGCAGAAGAACAGTCCAACAATGGTAGATATGACGATT TCCAGAACTTAGAAATGCCTGTATAGATGTCCTCAAGGAACTTGTACTTTTGAGTCCCCATGATTTTCTTCATACT

CATCGAACAACAAGGCCATGACAGATCCCTCCAGAAAGTATTTAACCAGCAGTAGAGAAAAGCAGCTGAGTTTGA AGCAGGACCTCACAGAAGGAAACCAGCAGGCAGCTTTCTTACTCAGACAATCAGGCTTCTGCAAAAAGAGGAAG ITTGGAAACTAAAGATGATATTCCATTTCGAAAAGTTCTTGGTAATCCGGGTAGAGGATCGATTAAGACTGTAGCA ATGTCTCCTCTGAAGATACATGGTCCTATCAGAATTCGAAGTATGCAGACTGGGATTACAAAGTGGAAAGAAGGA TCCTTTGAAATTGTAGAAAAAGAGAATAAAGTCAGCCTAGTAGTTCACTACAATACTGGAGGAATTCCAAGGATAT TTCAGCTAAGTCATAACATTAAAAATGTGGTGCTTCGACCCAGTGGAGCGAAACAAAGCGCGCCTAATGTTAACTC GCAAGATAACAGCTTCTTGTCTATTGACAAAGTACCAAGTAAGGATGCAGAGGAAATGAGGTTGTTTCTAGATG CAGTCCATCAAAACAGACTTCCTGCAGCCATGAAACCGTCTCAGGGGTCTGGTAGTTTTGGAGCCATTCTGGGC **GGAAGTGGAATAGCTCGGACGATTCCTTTGACATCTACTTCAACACCCTCTTAGATCAGGGTTGCTAGAAAAT**

>SGPR430 SEQID 6

L

OGGGGGTS COMBOI

>SGPR496 1 SEQID

ACTGCATCATAGACCAAATCTTCACAGGTGGCCTGCAGTCTGATGTCACCTGTCAAGCCTGCCATGGCGTCTCCA <u> AGGAACTGCGGGTTATCTACCAGTGCTTCGTGTGTGGAACCCCAGAGACCAGGAAAAGCAAGGCAAAGTCC</u> CCCAACCTGGGAAACAACCAAACCAGAATTAGAACTGCTGGGGCACAACCCGAGGAGAAGAAGAATCACCTCCA GGGGAAGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGAAGGTGGACGCCACCGAGGAGGTGGAGGACG COGATOCOTOTOCOGOTOGOAGTOGTOGOGOCOGOCOGOCOCOGOCOCOGOCOCOAGACOCOGOCTOGTA <u> 2TGCACCTGGTGTGGATACATGCCCGCCATTTAGCAGGGTACAGGCAACAGGATGCCCACGAGTTCCTCATTGC</u> TGGTCATCCACGTGAGTGTGAGCCAGGATTGATGACAAAAATAGAAGAGGATTGGAAGACAGTGAGCCAG GTGCCAAACTCTTCAATAATGATGGAGTCTGTTGTTGCCTGCAAAAACGGGGGCCAGTGAACATTACATCAGTGT 36ATGAATTACCTTTTGGTGTAATTGGTTCTAATATTGGTGATGCACATTTTCAAGAATTCAGGGCTGGAATCTCC FGGAAGCCTGTGGTAGATCCTGATGACCCCATTCCTCAGTTCCCTGATTGCTGCAGCAGCAGCAGCAGCAGGAGT SCGGGGAAGGTGGACGCCGCTGGGAAGGTGGAGACGGCGGGGGGTCCGGGCCGCCGCCGGCTGAGCT 36AGCCCGAACCCGAGCCGGTCCGGGAGGCGGAGCAGGAGCCGAAGCAGGAGCTGGAGGATGAGAACCCAG SATGTGGATTTTGCCGTGGGCCACCAGGCTGTTCTCACGTGAACAGCTTTAAGGTGGGAGAGAACTGGAGGC **ATACTGCTTTATGTGAAGGACTATGTATATGACAAAGACATTGAGCAAATTGCCAAAGAAGAGGGAGAGAGG** SCTTTACGATCGGTTTAAGAGGACTCATCAATCTTGGCAACACGTGCTTTATGAACTGCATTGTCCAGGCCCTCA CTGGTCTGTGAGATGTCGTCGTGTTTCGGGAGTTGTATTCTGGAAACCCGTCTCCTCATGTGCCCTATAAGTTA STGTGAGTCCCAGGACCTTACAAATATCAGTTTTTGTGTTATCAGAGAAATACGAGGGTATTGTTAAATTTGAATC GCATCTGCCATGTGTGTGGCACCCATCTGAACAGACTCCACTCTTGCCTTTCCTGTGTCTTCTTTGGCTGCTTC TTGAAATTACAAGCCTCCACCTCAACAGAGGTTTCTCACCAGCAGTGTTCAGTGCCAGGCCTTGGTGAGAAATI CCCACACGCCGATACTGAGAGATTTCTTTCTCTGACAGGCACCGATGTGAGATGCCGAGTCCCGAGTTGTGT <u> ATGACACTACTTGCTCCCTGGTACACAGGCCCCATGATCCCCATGGATGTTAATGAGCCCAGCTCCGTGACCAC</u> 4CGGAGAAACACATTCACGAGCACGCAGAGACGAAACAACACACTTAGCAGTAGACCTGTATTACGGAGGTAT **GECTCCTACCCTCAGCTCTAGCCTGCAGCATATCTCCTCATTCCTGGCCACTGGTAAGAAACTTTCCCTCCATT**

GGGAGGGAGAGCAGTGTGAACGGGGAAAGCCACATACCAGGAATCACCACCCTCACGGACTGCTTGCGGAGGT GGCGCAAGATCACTACATACATTTCCTTTCCTCTGGAGCTGGATATGACGCCGTTTATGGCCTCAAGTAAAGAGA GCAGAATGAATGGACAATTGCAGCTGCCAACCAATAGTGGAAACAACGAAAATAAGTATTCCTTGTTTGCTGTGG TTAATCACCAAGGAACCTTGGAGAGTGGCCACTATACCAGCTTCATCCGGCACCACAAGGACCAGTGGTTCAAG 1GTGATGATGCCGTCATCACTAAGGCCAGTATTAAGGACGTACTGGACAGTGAAGGGTATTTACTGTTCTATCAC SCACGATAGACCCATGCTGGGACATTAGTTTGGACTTGCCTGGCTCTTGCACCTCCTTCTGGCCCATGAGCCCA **AAACAGCTCACAATGAATAAATTACCTGTGTTGCCTGTTTTCATTTCAAACGGTTTGAACATTCAGCGAAACAGA** TTACGAGGCCAGAGCACTTAGGAAGCAGTGCCAAAATCAAATGTGGGTAGTTGCCAAAGCTACCAGGAATCTACC

SGPR495 SEQID 8

GCTTTGTCAGAAGGCACCTCGATTTAAAGATTTCCAGCAACAGGACAGTCAGGAGCTTCTTCATTATCTTCTGGAT GAAGACTCTTCAGATGATATTGCTGTAGGTTTAACTTGCCAACATGTAAGTCATGCTATCAGCGTGAATCATGTAA **AAGAGTCAACTAATTCATGACCGAAAATGTATTAGAAAATTGTCATCTGGAGAAACTGTCACATACCAGAAAATG** -ACTGATGACAGTGAAAAAAGAAGCCAGCCATTCTGAAAGCAATGTTGATGCTGACAGTGAGGCCTTCAGAATCTGA **AAGTECTTCAAAGCAGACTGGGCTGTTCAGATCCAGTAGTGGATCCGGTGTGCAGCCAGATGGACCCCTTTACC** TCAAGATTTTTCCTTCCTCAGACTCTCAGCTGGACCCATTGGTGGTGGAACTTTCAAGGCCTGGACCACTGACCT CAGCCTTGTTCCTGTTTCACAGCATGAAGGAGACTGAAAAAGGACCACTTTCTCCTAAAGGTTCTTTTAATCA IAGTACTTACTTCTGATATTTGGTTGTGCCTCAAGTGTGGCTTCCAGGGATGTGGGTAAAAACTCAGAAAGCCAAC AAACATGCTTCTAAAACAACAAGTGCATTTCTAGAATCATGAAACTTTGTGAAGAAAAATGTGAAAAACAGATG STGTTATGAATGTGATGAAAAATTATCAACGCATTGTAATAAGAAGGTTTTGGCTCAGATAGTTGATTTTCTCCAG GCAGTGAGGACAGAAGAAACAAAGCGAATACAAGCTAGCATTCTAAAAGCATTTAACAACCCAACTACTAAAACT -CGATACAGTGGCAATGTTACTATAGAAAATATTCATCAACCTAGAGCTGCCAAGAAGCATTCTTCATCTAAAGA1 ATGCGGGTGAAAGATCCAACTAAAGCTTTACCTGAGAAAGCCAAAAGAAGTAAAAGGCCTACTGTACCTCATGA CTCTGTCAGCAGGTAAACTGCTGTACACCAAGGAGACTGACAGTGGTGATAAGGAAATGGCAGAAGCTATTTCT

GAACTTCGTTTGAGCAGCACTGTAACTGGGGATCAAGATTTTGACAGAGAAAATCAGCCACTAAATATTTCAAATA 4 GAA G G A G TITTATA CTAATG C C A G C A A TIGCI C A TITCI G C I GITC C A G C T G T C T C C A C T G C T G A A <u> ATAACTACTTCTAAAGAATGTTCAATTCAGTCCTGTCTACCAGTTTACATCTATGGAATTACTAATGGGAATA</u> <u> AGATITICATCAGGCTGGCTTGAGTCTTCGTAAAGTAAACAGACATGTAGATTITICCACTTATGCTCGATTTTAGCAC</u> CATTCTGCTCTGCTACTTGTAAGAATGCAAGTGTGGGAGATAAAGTTCTCTACGGTCTCTATGGCATAGTGGAAC CATAACACTAAAAAGAAAAATGTGCCTGGTTTGAAAGCGGCTGATAGTGAATCAGCAGGCCAGTGGGTCCATGT ATTIATGITITITAGAGGGAAGCATTIGAGGTCTTATAGTCCCCAAAATGCTTTTCAGACCCTTTCTCAGAGCTA **4TAGTGGCTCGATGAGAAGGCCACTACACTGCTTATGTGAAAGTGAGAACACCCTCCAGGAAATTATCGGAA**

SGPR407 SEQID 9

FIG. 1K

TGGCTGGTGTTGGTGCCTCTGAAACTGACAGGAAGTCCCCACAGATGGAGGGCCCAGGAAGAGGGGCGCTGGCCA GAACCACTCAGGCAGCATCCACTGTGGCCACTACACAACCCTGTGCCAGTGCCAGACTGGTTGGCACGTTTACA ATGCCCTTTGTGATACCGAGCAAAACCTTGCCATGGGACCCACTGGAACTCAAGATTTGTTATCAGCAAAATCGC
 IATGGGAGCGGCTACACCTTGAAATCAACCACGGAGGCCGCGGGGCTCCACCAGTCCCTGCCCATGGTCCAGC
GCTGCAGCTGGTGTCTCCAAAGGGTCACCATGAGGCGGGTTATGGGTGTGCAGGACAAAGCTGGAAACAGGAA ATGGAGTATCCAGTCCCATACTTTAGATCCCCGAACAGGACTCTGATCCCAGAGAGAATTTGGTCAAACCCATTA ATGTGGAAGCGTTATCTGGAAGAACAAGAGGACAGCAAGATGGTGGATCTGTTGTGGGCCAGATGAAAAGTTA AGAGTTAGAGAATGCCTCAGGGACTTTGCCAGTGACAAAGTCGGAAGTCCTGTCTACCAGCTGTGTGCCTTTG ATGACTCTTGTGTCTCCCCTAAACACGCTGCGGGACACAGAAGGAATAGAACTCACAGTTATGAAGGCTCTAGTT SCTTGCAGACGGCCACCTTCTCACTCTGTCTTCACAGACCTCCTTCTGGGCATGTCTGGATCCTGATCTTCT **CCTCTCCACCCCACCAAGGGGAGTGCTCTGCTAAAAGAGTCTGAGTTAAATGATGCTGACTGGGCCAACCTA AGTTACCAGAACCTGGAGGTTTGGAAAAGAAACATGAAGAGCTGAGACTCAGACCTCTGAAGGAGGAGTACCAT CCATATCCCTCCCCCGACCCATCAAACTTTCCTACCTTCTTACGCTGTCTGAATGCTTTCTCTGCAGCTGTCTTCT CCCAAGAAAGGATTTGCTGGGGGCAAGGTGTCTCTGCGGGATTGTTTAAGCCTTTTCACCAAGGAAGAAGAGCT CCAGATGCTGCTGCTGGGGCAAAGACCTGTGATAGGTGATACAGTCAGCAACAGCCAGACAACTAGGGACAAG **ATCTCCCACAGCCCTCATGGCATAAGCCCGAGGGCTTAAAGCCAGCAGGATACCCAAGAGTTCCTGACATTCCT**

AGTGGGATGGAGCCACAGAAGTCTGCACCATTTGCAGCAGGGAAGGGTCTGGCCCCTCCTCTTCCTGTGTGCAA ATGCCCCAGAGTTTTTACTGGGGTTTTCCTGCTGGAGGGAACTTGTCTGCTTTAGAAATGCTGCCTGATGGACCA GCACCAAGGACGTTTCTTCAGAAGAAAAGCTGTCTCTTTCCCCTGTTCTTTACATTCTTTTGCATAAGGCAGGTA <u> AACTCTTCCAGCCTGATGCTCATGGATTTCTAGTGAAGAAAGTTCATGCTCCAACAAGGGGGCATCGTGTTTATCAT</u> GGAACCAAGACAGCTGGGTGGGAAGGGCTCCCTGTCAAAACTCCAACCAGCCTGTGCACTGGGAGGAATGAAC CCAAGGACAAATTCATTCCCCAAGGACAAATTTGTCCCCAAGGACAAATTGAAGGTGATATTGTCCCTGCTGACA CCTGAGATTCAAACTACGAGTTTACAAATTTGAGGAAGAGCTTTGGTCCAGGGCAGGCTTGGGGGAAGAAGTG ACAACCACTCATCTAGGCAGATGCCCTGGGGTGCCGCTGGGGTGGCATGCCAGCATCCATGTAAACTGCCAG TCCCTGTCTCAGTTTTTCCTCAATGATTCTCAACCAGAGGAAGCAATACCTCCTCAATCCCTGCTCCCGGGTTCC AATTGTTGCAGAGTTGACACCTCCAAAATTGTCATTTGGTTTCCTGAACACAGGTTCAGAGTTCAGTACTTCCTACT ATGTATGAACTAGACCGATTATTT

SGPR453_SEQID_10

FIG.

1L

GTCATCAGGACTAAGTGGTGGAGCATCAAAAGGTAGAAAGATGGAACTTATTCAGCCAAAGGAGCCAACTTCACA -ACATTAAGTGCCATCAAAAGTCAAAATTATCACTGCACAACTCGTAGTGGGAGGTTTTTACGGTCCATGGGTACA **AAGAAGAACCATTTCAGGAGAAAATAGTAGTAAAAAGAGAAGTAAAAGAAAAGACGGCAGGAATTGGAGTATCAAG** FAAAGCTTGATCTGAACCAATGGCTGGCTATGACTGCTAGCGAGAAGACAAGATCTTGTAAGCATCCACCAGTCA GTACATTICICITITGICATGAATTGCATACTTTGTTCCAAGTCATGTGGTCTGGAAAGTGGGCGTTGGTCTCACCA GGCACAGGAGAAGGATACTAATGGGTAAAATCTTTCGAACATGGTTTGAACAATCACCCATTGGAAGAAAAAGC GAAATGGCACTGTGTGGACTGCAACACGACCGAGTCCATTTGGGCTTGCCTTAGCTGCTCCCATGTTGCCTGTG SAAGATATTTGAAGAGCATGCACTCAAGCACTTTCAAGAAAGCAGTCATCCTGTTGCATTGGAGGTGAATGAGA TGTACGTTTTTTGTTACCTTTGTGATTATGTTCTGAATGATAACGCAACTGGAGACCTGAAGTTACTACGACG AAATAGTTTCTGTTCAGGTGCCAGCACAAACGCCAGCATCACCAGCAAAAGATAAAGTACTCTACCTCAGAAA SAAATTTGGGAAATACTTGCTATATGAATTCTGTTCTTCAGGTGTTGAGTCATTTACTTATTTTCGACAATGTTTT ATGCTAGCAATGGATACGTGCAAACATGTTGGGCAGCTGCAGCTTGCTCAAGACCATTCCAGCCTCAACCTCA ATGAAATATCTCAAAAAGTCAGTGACTCCTCAGTTAAACGAAGGCCAATAGTAACTCCTGGTGTAACAGGATTGA <u> GGTGATGATTCTTATTTCTTACATGACGGTGCCCAATCTCTGCTTCAAAGTGAAGATCAACTGTATACTGCTCTTT</u> TTGCTATGCTACACTCAGTGTGGAGACTCATTCCTGCCTTTCGTGGTTACGCCCAACAAGACGCTCAGGAATTT CTTTGTGAACTTTTAGATAAAATACAACGTGAATTAGAGACAACTGGTACCAGTTTACCAGCTCTTATCCCCACTT GATTCCAAACTAAGCATGTGCACTATGGATGAAGTATGCAAGGCTCAAGCTTATATATTTTTATACCCAACGAG CTCAAAGGAAACTCATCAAACAAGTTCTGAATGTTGTAAATAACATTTTTCATGGACAACTTCTTAGTCAGGTTACA TACTGAGAATGGACATTCTAAACTTTTGCCTCCAGAGCTCCTGTTGGGGAGCCAACATCCCAATGAAGACGCTG GTCTTGCATGTGACAACAAATCAAATACCATAGAACCTTTCTGGGACTTGTCATTGGAGTTTCCAGAAAGGTATC CTTTAGAAGGAAAAATCTACGTATGTGACCAGTGTAACTCAAAGCGTAGAAGGTTTTCCTCCAAACCAGTTGTACT **GTCAGGACGTAATAACCGAGAGAAGATTGGTGTTCATGTTGGCTTTGAGGAAATCTTAAACATGGAGCCCTATTG** STECAGEGAGACCCTGAAATCCCTCAGACCAGAATGCTTTATCTATGACTTGTCCGCGGTGGTGATGCACCATG AATGCAGTGGAAAAGATATTGCTTCCCAGCCATGTCTGGTTACTGAAATGTTGGCCAAATTTACAGAAACTGAAG SGAAAGGATTTGGCTCAGGGCACTACACTGCCTACTGCTATAATTCTGAAGGAGGGTTCTGGGTACACTGCAAT ATACCTCGTCTAATGAAATCCTTAGCTGA

SGPR445 SEQID 11

<u> AAATACAGAAGGGAGGAAAATGCAGAAATTTATCTGTAAGAGGAATTACAAATTTAGGAAATACTTGCTTTTTAAT</u> SAAGACTCTTCAGATGATATTGCTGTAGGTTTAACTTGCCAACATGTAAGTCATGCTATCAGCGTGAATCATGTAA ICAAGATITITCCTTCCTCAGACTCTCAGCTGGACCCATTGGTGGTGGAACTTTCAAGGCCTGGACCACTGACCT <u> ATGCGGGTGAAAGATCCAACTAAAGCTTTACCTGAGAAAGCCAAAAGAAGTAAAAGGCCTACTGTACCTCATGAT</u> AAACATGCTTCTAAAACACAAACAAGTGCATTTTCTAGAATCATGAAACTTTGTGAAGAAAAATGTGAAACAGATG CAGCCTTGTTCCTGTTTCTTCACAGCATGAAGGAGACTGAAAAAGGACCACTTTCTCCTAAAGGTTCTTTTAATCA **GTGTTATGAATGTGAAAAAAATTATCAACGCATTGTAATAAGAAGGTTTTGGCTCAGATAGTTGATTTTCTCCAG** IAGTACTTACTTCTGATATTTGGTTGTGCCTCAAGTGTGGCTTCCAGGGATGTGGGTAAAAACTCAGAAAGCCAAC SCTTTGTCAGAAGCGGGTGCATCTACATTTAATATAA

>SGPR401 1_SEQID_12

GAGCAGTTTCCAATCAATGAACACTATTTCGGATTGGTCAATTTTGGAAACACATGCTACTGTAACTCCGTGCTTC ATGACTGTCCGAAACATCGCCTCCATCTGTAATATGGGCACCAATGCCTCTGCTCTGGAAAAAAGACATTGGTCCA TTGCTGACGTGCCTGGCGGACCTTTTCCACAGCATTGCCACACAGAAGAAGAAGGTTGGCGTCATCCCACCAAA GAAGTTCATTTCAAGGCTGAGAAAAGAGAATGATCTCTTTGATAACTACATGCAGCAGGATGCTCATGAATTTTTA AGGCATTGTACTTCTGCCGTCCATTCCGGGAGAATGTGTTGGCATACAAGGCCCCAGCAAAAGAAGAAGGAAAAC

4ATTATTTGCTAAACACTATTGCGGACATCCTTCAGGAGGAGAAGAAACAGGAAAAAACAAAATGGAAAATTAAAAA ATGGCAACATGAACGAACCTGCGGAAAATAATAAACCAGAACTCACCTGGGTCCATGAGATTTTCAGGGAACGC GGCCCTGCACCTAAAGCGGTTCAAGTACATGGAGCAGCTGCGCAGATACACCAAGCTGTCTTACCGTGTGTCT TACCAATGAAACTCGATGCTTGAACTGTGAAACTGTTAGTAGCAAAGATGAAGATTTTCTTGACCTTTCTGTTGA TGTGGAGCAGAATACATCCATTACCCACTGTCTAAGAGACTTCAGCAACACAGAAACACTGTGTAGTGAACAAAA rcctctggaactccggctcttcaacacctccagtgatgcagtgaacctggaccgcatgtatgacttggttgcg STGGTCGTTCACTGTGGCAGTGGTCCTAATCGTGGGCATTATATCACTATTGTGAAAAGTCACGGCTTCTGGCTT TGTTTGATGATGACATTGTAGAGAAAATAGATGCTCAAGCTATTGAAGAATTCTATGGCCTGACGTCAGATATAT **ATATTATTGTGAAACATGCTGCAGCAAACAAGAAGCCCAGAAAAGGATGAGGGTAAAAAAGCTGCCCATGGTCT** CAAAAAATTCAGAATCTGGATATATTTTATTCTATCAGTCAAGAGAGTAA

>SGPR408 SEQID 13

AGATATGAGTACTTTTATTGATGTTGAAGATGAGAAATCTCCTCAGACTGAAAGTTGCACTGACAGTGGAGCAGA SCAAACAGAACAGGCTGATCTTATAAATGAGCTATATCAAGGCAAGCTGAAGGACTACGTGAGATGTCTGGAATG 'GGTTATGAGGGCTGGCGAATCGACACATATCTTGATATCCCATTGGTCATCCGACCTTATGGGTCCAGCCAAGC SAAGCAGAGGATATTATTCTAGTGCTTTCGCAAGTTCCACAAATGCATATATGCTGATCTATAGACTGAAGGATCC
 FAGTGAGGCTTGGCAGCATGATGTACAAGAACTATGCAGAGTCATGTTTGATGCTTTGGAACAGAAATGGAA
GGTACAGCTTCGATGATCAACATGTCAGCAGGATAACACAAGAGGACATTAAGAAAACACATGGTGGATCTTCAG AATGCATTATATAAGTGGGAATTTGAAGAATCTGAAGAAGATCCAGTGACAAGTATTCCATACCAACTTCAAAGGC CTGAAAAGATTCGATTTTGATTATACAACCATGCATAGGATTAAACTGAATGATGATGACATTTCCCGAGGAAC GCTGGAGGATTCCAGTGCTGGGGAAGACAGTGTTCATGACAGGTTTATAGGTCCGCTTCCAAGAGAAGGTTCTG SAACGTTGTAAGAAGAAGTGTGATGCACGGAAGGGCCTTCGGTTTTTGCATTTTCCTTATCTGCTGACCTTACAG AAATGAAGGTAGTTGTCACAGTGATCAGATGAGCAACGATTTCTCCAATGATGATGGTGTTGATGAAGGAATCTG <u> ATGGTGCCCGGCGAGGAGCAACTGGTCCCGAAAGAGGCACCACTGGATCATACCAGTGACAAGTCACTTCT</u> SGGACTAGTAAACCAAGCAATGACTTGCTATTTGAATAGCCTTTTGCAAACACTTTTTATGACTCCTGAATTTAGG <u> CTGTTATGGCTCATTCTGGGAGCGCTGCTGGTGGTCATTATTATGCATGTATAAAGTCATTCAGTGATGAGCAGT</u> CGACGCTAATTTTGAGCCAGGAAAGAAGAACTTTCTGCATTTGACAGATAAAGATGGTGAACAACCTCAAATACT IGGGTTCTACCAGTGATTATGTCAGCCAAAGCTACTCCTACTCATCTATTTGAATAAATCAGAAACTGGATATGI

4GGTTGTATTGGAAAGCAGTAGTGTGGACGAATTGCGAGAGAAGCTTAGTGAAATCAGTGGGATTCCTTTGGATG CTGTGGAAGCTATTCTAGAAGAAAGCACTGAAAACTCAAAAGCTTGTCACTGCAGCAACAGCAGGATGGAGATA CAGCATCAGTGGATAATAGAGAACTTGAACAGCATATTCAGACTTCTGATCCAGAAAATTTTCAGTCTGAAGAACG GTTGGAAGAACAAGAAAAGAGACAACGAGAAATTGAGCGCAATACATGCAAGATAAAATTATTCTGTTTGCATCCT ATATGATGAGAGTGGCAAGAGTAGGGGAGAAATGCAGTACATGTTTTCAAAGCTGAACCTTATGCTGCAGATGA TTAGAGCCCTTTGTTGGAGTTTTGTCCTCTCACTTCAAGGTCTTTCGAGTGTATGCCAGCAATCAAGAGTTTGAG TAGAGCTCAGTATTGACAGGTTTCGTCTAAGGAAAAAAACATGGAAGAATCCTGGCACTGTCTTTTTGGATTATC ACAAAACAAGTAATGATGGAAAATAAATTGGAGGTTCATAAGGATAAGACATTAAAGGAAGCAGTAGAAATGGCTI ICTAGAACGGTCATATGAAGGAGAAGAAGATACACCAATGGGGCTTCTACTAGGTGGCGTCAAGTCAACATATAT IACAATGATTTGCGTCTTCTCAGTGTCTCCAGTAAAACCCTGAAAGCTGAAGGATTTTTAGAAGTAACAAGGTGT **ATCAGACTCAGATGTGAATAATGACAGGAGTACAAGTTCAGTGGACAGTGATATTCTTAGCTCCAGTCATAGCAG** IGATACTTTGTGCAATGCAGACAATGCTCAGATCCCTTTGGCTAATGGACTTGACTCTCACAGTATCACAAGTAGT ATAAGATGATGGATTTAGAAGAGGTAATACCCCTGGATTGCTGTCGCCTTGTTAAATATGATGATGAGTTTCATGATTA STTTGATCTGCTGTTGGAGACGAGAAAGCCTGATCAGGTTTTCCAATCTTATAAACCTGGAGAAGTGATGGTGAA TETTGAAAGCTCCGAGACTTTGGATTACCAGATGGCCTTTGCAGACTCTCATTTATGGAAACTCCTGGATCGGC SAAAGCTGGAGGCGATTCTGGTAATGTGGATGATGACTGTGAAAGAGTCAAAGGACCTGTAGGAAGCCTAAAGT 4GAAGAACGAAAGCAAATGAAGGGAAAAAAAAAACATGGGATACAGCAGAAGAAGACTCTGGAACTGATAGTGA **AGGTTCTGGGGAAGGACATAAATGGTTGATGGTGCATGTTGATAAAAGAATTACTCTGGCAGCTTTCAAACAACA** ATATTTATGAAGAAGATATTAATATTTCCAGCAACTGGGAGGTTTTCCTTGAAGTTCTTGATGGGGTAGAGAAGAT SAAGTCCATGTCACAGCTTGCAGTTTTGTCAAGACGGTGGAAGCCTTCAGAGATGAAGTTGGATCCCTTCCAGG SAATCCTAAAGTTTCTACCCTGAATGTCTGGCCTCTTTATATCTGTGATGATGGTGCGGTCATATTTTATAGGGAT 4CAGAATTCAAACAACTGATTTCAAAGGCCATCCATTTACCTGCTGAAACAATGAGAATAGTGCTGGAACGCTGC ATATTGAATTTGCTAAGGGTAGAGGAACATTTCCCTGTGATATTTCTGTCCTTGATATTCATCAGGATTTAGACTG **4TGCAAATACAATCAGATTATTTGTTTTGCTACCTGAACAATCCCCAGTATCTTATTCCAAAAGGACAGCATACCA** 4GCGTCCGGCTGAATGAGACACTTTCATCATTTTCTGATGACAATAAGATTACAATTAGACTGGGGAGAGCACTT **4AAGATCTGACTCAAGACTGA**

TAAAACGACTGAAGGATGCTTTCAAGAGGACCTGTGGACTCTCATATTACATGGGCCAGCACTGCTTCATCCGGG CAGTTACGTGAATACTACAGAAGAGAAATTTTCAGACAACATTTCTACTGCATCTGAAGCCTCAGAAACTGCTGGC CAGCTGATTCATGGAAGAGACTATGAAATGGTCCCAGAACCTGTGTGGAGAGCACTTTATCACTGGTATGGAGCA AGTGATACTCCTACTTTCTACCAAACTCTGGCTGGAGTCACACATTTGGAGGAATCAGACATCATTGATCTTGAGA TITITCTAAACAAAGATGCTTTTACTTTCTCTCGATGGCTTCTATCTGGAGGTGTGTATGTTACCCTCACTGATGAT CACCTATTCGTCCATCTCTAAGTGAAGGTTTGTTTAATGCTTTTGATGAAAATCGTGACAATCACATAGATTTTAAG GGACAACCGCACTGATGATATTCCTGAATTACATATGGATCTCTCTGATATTGTAGAAGGCATACTGAATGCACAT ATTATTAGAGGATGGTTAGAACGAGAGGAGGTATGGTCTGCAAGCAGGACACAACTGGTTTATCATCTCCATG CTTCTCTTCCTGAGACAGCAGCCTGCCACTCGGACACAGCAGTCTAACATCTGGGTGAATATGGGAAATGTACCT CACGAATATCTATCTCAAAGGCTGCGCATTAAAGAGGAAGATATGCGCCTGTGGCTATACAACAGTGAGAACTAC STTACTCTTCTGGATGAGGATCATAAATTGGAATATTTGAAAATCCAGGATGAACAACACCTGGTAATTGAAG ATGGGTGCCAAGGAGTCACGGATCGGATTCCTCAGCTACGAGGAGGCGCTGAGGAGGAGTTACAGATGTAGAGC GACACCACAAAGATGGGTCATCTTACTCTGGAAGACTATCAGATCTGGAGGTGTGAAAAAATGTTGCCAATGAG TTTTGAACCTCCTTTTCCAGGTGTGTCACATAGTTCTGGGGTTAAGACCAGCTACTCCGGAAGAAGAAGAAGACAA CAGTGGTGGCAACAGTGGAAAGAATATGTCAAATACGATGCCAACCCTGTGGTAATTGAGCCATCATCTGTTTG GTAAAGTCCCAGATACACTCAGGAAGTGTTTCTCAGAGGGTGAAAAGGTAAAACTATGAAAAGTTTAGAAATTGGC AGCGGCTTTCTGTATTCTGCCACACACAGGGGCAGATGTTTGCTTTGCTCGACACATAACACTTCTGACAATAAC AACCAGTGTTTGCTGGGAGCCAATGGGAATATTTTGTTGCACCTTAACCCTCAGAAACCAGGGGGCTATTGATAAT CAGCCATTAGTAACTCAAGAACCAGTAAAGGCTACATTAACACTAGAAGGAGGAGGATTAAAAACGAACTCCA TAGTCTTTTTCAAGTGAATCTGGGAACTATGTTATACGGGAAGAAATGGAAAGAATGCTCCACGTGGTGGATG CCCACAGAAAAGGGAGCCACAGGTCTAAGCAATCTGGGAAACACATGCTTCATGAACTCAAGCATCCAGTGTG AAGTECTTGEGGATGGAGTGCCTCCAAAGGTTGCTGAGGTGATTTACTGTTCTTTTGGTGGAACATCCAAAGGG AACGCTATTGGTTATTGAAGGCTCAATCCCGGACTGGACGATTTGATTTAGAGACATTTGGCCCATTGGTTTCAC GAGATATCCTGTGGGTTATCAGCCTGTTGCAGGGGACCCCTGGCTGAAAGACAAAAATTTTGCTTCAAGGTATTT GATGTTGACCGTGATGGAGTTCTCTCCAGGGTTGAACTGAGAGACATGGTGGTTGCACTTTTAGAAGTCTGGAA **AATGGAGGAAAATACTCATTTGGAACTGCAGCCCATCCTATGGAGCAGGTCGAAGATAGAATTGGAAGCAGCCT** CTGCACTTCAATAATTTAATAGTTGGACTTGTCCTCCTTACAAGAGGCAAAGATGAAGAGAAAGCAAAATACATTI TCTCCGAATGCACCTTTAAAGCGGGTATTAGCCTATACAGGCTGTTTTAGTCGAATGCAGACCATCAAGGAAATT >SGPR480 SEQID 14

CTCAGGACAACCAAAAAGTACGACTCTCAGTGAGTGGATTTTTGTGTGCATTTGAAATTCCTGTCCCTGTGTGTCTCC SAACTTCACAAATGGAATGGTTAATGGTCACATGCCATCTCTTCCTGACAGCCCCTTTACAGGTTACATCATTGCA CTGATTATTCACCTTAAGCGATTTCAATTTGTAAATGGTCGGTGGATAAAATCACAGAAAATTGTCAAATTTCCTCG AGAACTTCTGGCTTTTCTCTTGGATGGTCTTCATGAAGATCTTAATCGAGTCCATGAAAAGCCATATGTGGAACTG SATTTGACCCTTTCAATTTTTTGTCTTTGCCACTACCAATGGACAGTTATATGCACTTAGAAATAACAGTGATTAAG STCCACCGAAAAATGATGAGGACAGAACTGTATTTCCTGTCATCTCAGAAGAATCGCCCCAGCCTCTTTGGAATG SCATGAAGCATGTGGCAATGGCTACAGCAATGGTCAGCTTGGAAACCACAGTGAAGAAGAAGACAGCACTGATGACC GCCCCATTAAAGCTTCGGTGGACCATAGCAAAATATGCTCCCAGGTTTAATGGGTTTCAGCAACAGGACTCCCA STGAGTGATCTCTGTGGACTTAATTCAGAACAAATCCTTCTAGCAGAAGTACATGGTTCCAACATAAAGAACTTTC TAGCGAGCCCACTCCCACCTCAGGAAGCTAGTAATCATGCCCAGGATTGTGACGACAGTATGGGCTATCAATAT <u> CCATTCACTCTACGAGTTGTGCAGAAGATGGGAACTCCTGTGCTTGGTGCCCATGGTATAGATTTTGCAGAGGC</u> 'GTAAAATTGATTGTGGGGAAGACAGAGCTTTCATTGGAAATGCCTATATCGCTGTGGATTGGGATCCCACAGCC STTCACCTTCGCTATCAAACATCCCAGGAAAGGGTTGTAGATGAGCATGAGAGTGTGGAGCAGAGTCGGCGAGC ATGTACTACTGTTCCAAGTGTAAGACCCACTGCTTAGCAACAAAGAAGCTGGATCTCTGGAGGCTTCCACCCATC GGAAAGTTTTGATCCAAGTGCTTTTTTGGTACCAAGAGCCCGGCTCTCTGCCAGCATAAACCACTCACACCCCA rggtatgaaggggcatatggctaaatgctatggtgatttagtgcaggaactttggagtggaactcagaagaatgt SCATTGATTGTTCCATGTACTGTGCATACCCGGAAGAAGACCTATATGATGCGGTTTGGATTCAAGTATCCCGG STTCTTCATCAAGAAAAAGTGGAACCAGCTGTCCCTCCAGCAAAAACAGCAGCCCTAATAGCAGCCCACGGACTI CTGGGGGGCGCCAACCAGAGTTGGTCACTCCTCAGGACCATGAGGTAGCTTTGGCCAATGGATTCCTTTATGA TTAGTAACACACAGCCACTGACACAGTATTTTATCTCAGGGAGACATCTTTATGAACTCAACAGGACAATCCCA1 CAATTGTTGTGGATTTGTTCCATGGGCAGCTAAGATCTCAAGTAAAATGCAAGACATGTGGGCATATAAGTGTCC AATTTCAGCTTCTAGTCCAACACAGACAGATTTCTCCTCTTCGCCATCTACAAATGAAATGTTCACCCTAACTACC SCAAGCCGAGCCCATCAACCTGGACAGCTGTCTCCGTGCTTTCACCAGTGAGGAAGAGCTAGGGGAAAATGAG
 AATGGGGACCTACCCCGACCAATATTCATCCCCCAATGGAATGCCAAACACTGTTGTGCCATGTGGAACTGAGAA
GGGGGATGAGCTCTCTGAGCCCAGGATTCTGGCAAGGGAGGTGAAGAAAGTGGATGCGCAGAGTTCGGCTGG SCATTACGTCACTTATGCCAAAAACCCAAACTGCAAGTGGTACTGTTACAATGACAGCAGCTGTAAGGAACTTCA 4AGGACAGTGATGGGCGACCAGACTGGGAAGTAGCTGCAGAGGCCTGGGACAACCATCTAAGAAGAAATAGAT

GCCAAAGACTGATGGCAAAAAGATGGCAGACACACAGCAGTATGGATGAAGACTTTGAGTCTGATTACAAAAGTA CCCGGATGAAATTGACACCGACTCTGCCTACATTCTTTTCTATGAGCAGCAGGGGATAGACTATGCACAATTTC CTGTGTTACAGTAA

>SGPR431 SEQID 15

GCCAGAGTTCGAGTCCTTCTTCAACAAGACCTTCGTGTTGGGCCTCCTTCATCAGGGCTACCACTCTGGACAG AAGTGAGTAACTTGCTGCAGAACATCTGGAAGGCCGAGCCTGCCACACTACTGCCTTCCCTGCAAGAAGTTTTTG TGGTGGAATCGGCGGAGCACTGGCTAGACGAGGCGCAGTGCGAGGCCATGTTTGACCTGACGACCCGGCTCAT GAGCGACCTTCTGACCGACTTTGTGCAATGCATCCCCAAGGGGAAATTGTCCATCACGTTCTGTCAACAGCTGG TCGAACGATAGGCCATTTCCAGTGCGTGTCCACCCAGGAAAGAGAGCTGCGGGAATATGTCTCCCAGGTGACAA SAAGCATCTCCACAGATGCATCATTTGAACCTTCTGTAGCATTGGCAAGCCTTGTGCAGCATATTCCTCTTCA CCTGGAGGGCCAGGACCCTTTCCAGCGGCAGGTGGGGCACCAGGTGCTGGAGGCCTACGCACGATACCACCG CAGAATGATTGACTGGCTATCCTGGCCATTGGCTCAGCATGTGGATACATGGGTAATTGCACTCCTGAAAGGACT SAAAACATGTCTGTCCAAGATCCAGCATCATCACCCAGTATACAAGATGGTGGTCTAATGCAAGCCTCTGTACCC GAAGGATGTAGCCATCCTGGACTACATTCACAACGGCCTGAAGCTGATTATGAGCTGTCCGTCGGTGCTGGATC GGCAGCTGTCCAGAAGTTTACTATTTTGATAGATGTTACTTTGCTGAAAATAGAACTGGTTTTTAATCGACTTTGGT SCATTTGATTGTTCCTCATGTGGTTAATTTGGTTCATTCTTTCAAAAATGATGGTCTGCCTTCAAGTACAGCCTTCT TAGTACAATTAACAGAATTGATACACTGTATGATGTATCATTATTCTGGATTTCCAGATCTCTATGAACCTATTCTG CTCGTACAAGTGACGGTGAGAAGACTTTAATAGAAAAAATGTTTGGAGGAAAACTACGAACTCACATACGTTGTTT TTCCTCTTGTGAGACCTGGTGCTCTTGCAGTTCTTTCTCACATGCTGCTTAGCTTTCAGCATTCTCCAGAGGCGTT ITAAATCTAAATGGGTGCAATTCATTAATGAAAAATTACAGCATCTTTTTGCCTTTCTGGCCCATACACAGAGGG STGAATACCTCAGATTTCTCCTTGACAGGCTCCATGAAGAAGAAAAGATCTTGAAAGTTCAGGCCTCACACAAGC CTTCTGAAATTCTGGAATGCAGTGAAACTTCTTTACAGGAAGTAGCTAGTAAAGCAGCAGCAGTACTAACAGAGACCC ATGGACAAGATCCTGGAGGGCCTTGTGAGTTCCTCGCATCCCCTGCCCCTCAAGCGGGGTGATTGTGCGGAAGG TCTTTAGCCTCCTGCAGGTAGAGGTGTTACGGATGGTGTGTGAGAGGCCGGAGCCGCAGCTCTGTGCCCGACT GATGATTACAGTTCTCATCAGGAGCCTTACTACGGATCCAAATGTAAAAGATGCAAGTATGACCCAAGCCCTTTG <u> AATCCAATTCTTTGGCGTCTTGCTTGTCTAGACTTTCTGGAAAATCTGAAACTGGGAAAACTGGTCTTATTAACCT</u> <u> AGGAAATACATGTTATATGAACAGTGTTATACAAGCCTTGTTTATGGCCACAGATTTCAGGAGACAAGTATTATCT</u> **AAGCATACGCACCTCGGATATTCTTTGAGGCTTCCAGACCTCCATGGTTTACTCCCAGATCACAGCAAGACTGT**

FIG. 1R

CATGTTCATTTCGGCCCAATGGATTTGATGACAACGACCCACCAGGAAGCTGTGGACCAACTGGTGGAGGGGGGT

3GAGGAGGATTTAATACAGTTGGCAGACTCGTATTTTGA

CAAAAGACAATAAACTATATTACAGGAACAAGAGTTGAATGCTCGAGCCCGGGCCCTCCAAGCTGCATCTGCTT

CAGAAAGTTGGTCTGTAGATGTTGACTTCACTGATCTTAGTGAGAACCTTGCTAAAAAATTAAAGCCTTCAGGGAC 4GTGGGCATTACTATTCTTATGCCAGAAATATCACAAGTACAGACTCTTCATATCAGATGTACCACCAGTGTGAGG CTCTGGCATTAGCATCCTCCCAGAGTCATTTACTAGGGAGAGATAGTCCCAGTGCAGTTTTTGAACAGGATTTGG SCAGAGATTCTTACTGGTGATAACCAATATTATTGTGAAAACTGTGCCTCTCTGCAAAATGCTGAGAAAACTATGC I GATGAAGCTTCCTGCACAAAATTGGTGCCCTATCTATTAAGTTCCGTTGTGGTTCACTCTGGTATATCCTCTGAA AAATCACGGAGGAACCTGAATACCTTATTCTTACTCTCGAGATTTTCATATGATCAGAAGTATCATGTGAGAAG **AAAATTACGAGCAGGTTTCCAAAGGACACAGCTTATGTGCTTTTGTATAAAAAACAGCATAGTACTAATGGTTTAA** FAATAAAGATGTACCTCAGAAACCAGGAGGTGAAACCACACCTTCAGTAACTGACTTACTAAATTATTTTTGGC1 SCATAGGCAGTCCTCCTAATGAGTTTTACTGTTCTGAAAACACTTCTGTCCCTAACGAATCTAACAAGATTCTTG

STACTTGTTTGCCTTGTTGCAAAACAGTAATAGGCGATACATTGATCCATCAGGATTTGTTAAAGCCTTGGGCCTG **AAAAGAATCCAGATGTGCGCAATATTGTTCAACAGCAGTTCTGTGGAGAATATGCCTATGTAACTGTTTGCAACCA** GTGTGGCAGAGAGTCTAAGCTTTTGTCAAAATTTTATGAGCTGGAGTTAAATATCCAAGGCCACAAACAGTTAACA SATTGTATCTCGGAATTTTTGAAGGAAGAAAATTAGAAGGAGACAATCGCTATTTTTGCGAGAACTGTCAAAGCA **3GCCACTACATCGCCCACGTGAAAGATCCACAGTCTGGTGAATGGTATAAGTTTAATGATGAAGACATAGAAAAG** FAGTGACTACATGCTGGGAGACGGCATCCAAGAAGAAAAAGATTATGAGCCTCAAACAATTTGTGAGCATCTCCA 'GACAGGCAAACTGGACATAAGAAAAAGCTGAATACCTACATTGGCTTCTCAGAAATTTTGGATATGGAGCCTTAT <u> AAAGGAAATCCGAATTGCTTGGTTGGTTGGTGAGCATATTTGGTTAGGAGAAATAGATGAAAAATAGTTTTCATA</u> SACACTGGACAACAGCAGGATGCTCAAGAATTTTCAAAGCTCTTTATGTCTCTATTGGAAGATACTTTGTCTAAAC ATGECCCCGCGCGTGCAGCTGGAGAAGGCGGCCTGGCGCTGGGCGGAGACGGTGCGGCCCGAGGAGGTGTC GCAGGAGCATATCGAGACCGCTTACCGCATCTGGCTGGAGCCCTGCATTCGCGGCGTGTGCAGACGAAACTGC 4CATCGATGATCCCAACTGTGAGAGGAGAAAAAAAACTCATTTGTGGGCCTGACTAACCTTGGAGCCACTTGT >SGPR429 SEQID 16

ATGGAGGGAAGAAATTACAACTAGGGATTGAGGAAGATCTAGAACCTTCTAAGTCTCAGACACGTAAAACCCAAG TGTGGCAAAGGAACTCATTGCTCTGGAAATGCATATATGTTGGTTTATAGACTGCAAACTCAAGAAAAGCCCAACA CTACTGTTCAAGTTCCAGCCTTTCTTCAAGAGCTGGTAGATCGGGATAATTCCAAATTTGAGGAGTGGTGTATTGA TAAAAGAATTGAAAATTCAGATCATGCATGCATTTTCAGTTGCTCCTTTTGACCAGAATTTGTCAATTGATGGAAAG ATTTTAAGTGATGACTGTGCCACCCTAGGCACCCTTGGCGTCATTCCTGAATCTGTCATTTTATTGAAGGCTGATG GGTTACCTGCTGGAGCTGAGCCCTATGAGTTTGTCTCTCTGGAATGGCTGCAAAAGTGGTTGGATGAATCAACAC CAGAAACACAGTATATTTCTGAGCCCAAACTCTGTCCAGAATGCAGAGGAAGGCTTATTGTGTCAGCAGCAGAGGG TCCAAAGGCTCCTGAGTTTCCAAGTTACAAAGAGTGCTGTTCACAGGGCAAGATTTTAGAAAGAGAAGGGGAAGA GAAATTTGTTAGAAAGCCTACAAGATGCAGCCCTGTGTCATCAGTTGGGAACAGTGCTCTTTTGTGTCCCCACGG CTACCAAACCTATTGATAATCACGCTTGCCTGTGTTCCCATGACAAGCTTCACCCGGATAAAATATCAATTATGAA TAAATAAAGATGAATCAAAGGAAGAAAGAAAGAAGAGGGGGGAATTAAATTAATGAAGATATTCTGTGTCCACA AAATGAAGCCTTACATAAGATGATTGCAAACGAGCAAAAGACTTCTCCCCAAATTTGTTCCAGGATAAAAACAGA
 AATGGCTGAGATGCGTAAGCAAAGTGTGGATAAAGGAAAAGCAAAACACGAAGAGGTTAAGGAGCTGTACCAAA
GCTAGCTCTTGAACAGCTGGATGAGCAAGATGGTGATGCAGAACAAAGCAACGGAAAGATGAACGGTAGCACCT **ACCTGCGTGAATACACTCAAGCCACCATCTATGTCCATAAAGTTGTGGATAATAAAAAGGTGATGAAGGATTCGG** AACCAATTGCAGATTATGCTGCAATGGATGATGTCATGCAAGTTTGTATGCCAGAAGAAGAGGGTTTAAAGGTACTG CTCCGGAACTGAATGTGAGTAGTTCTGAAACAGAGGAGGACAAGGAAGAAGCTAAACCAGATGGAGAAAAAGAT GTGTAAGGAATGTGTAGTAGAACGTTGTCGCATATTGCGTCTGAAGAACCAACTAAATGAAGATTATAAAACTGT CAAATGATACAAAAGCTCTTTGTTGTGGATCATGTAATTAAAATCACGAGAATTGAAGTGGGGAGATGTAAACCCTT <u> AAGTTATTCGCCGAAGTATGCGACATAGAAAAGTTCGTGGTGAGAAAGCACTTCTCGTTTCTGCTAATCAGACGT</u> SAGGATATCTGAATATGCAGCTGACATTTTCTATAGTAGATATGGAGGAGGTCCAAGACTAACTGTGAAAGCCCT CCGTGTCTCAGTAACTGGCCAGAGGATACGGATGTCCTCTACATCGTGTCTCAGTTCTTTGTAGAAGAGTGGCG TGGTGAGTTATGCATATCTGAAAATGAAAGAAGGCTTGTTTCTAAAGAGGCTTGGAGCAAACTGCAGCAGTACTT

FIG. 1T

>SGPR503 SEQID 17

ATGCTGAGCTCCCGGGCCGAGGCGGCGATGACCGCGGCCGACAGGGCCATCCAGCGCTTCCTGCGGACCGGG GCGGCCGTCAGATATAAAGTCATGAAGAACTGGGGAGTTATAGGTGGAATTGCTGCTGCTCTTGCAGCAGGAAT **ATATGTTATTTGGGGTCCCATTACAGAAAGAAAGAAGCGTAGAAAAGGGCTTGTGCCTGGCCTTGTTAATTTAGG**

GTACAGATGGCAGATCTCATCTTGAAGAACAGGATGCTCACGAATTATTCCATGTCATTACCTCGTCATTGGAA AGCCTTTCACTAAGTATTCCAGCCGCCACATGGGGTCACCCATTGACCCTGGACCACTGCCTTCACCACTTCATC TCATCAGAATCAGTGCGGGATGTTGTGTGTGACAACTGTACAAAGATTGAAGCCAAGGGAACGTTGAACGGGGA AAAGGTGGAACACCAGAGGAGCACTTTTGTTAAACAGTTAAAACTAGGGAAGCTCCCTCAGTGTCTCTGCATCCA GTGGCTGTGGGTCTCCGATGACACTGTCCGCAAGGCCAGCCTGCAGGAGGTCCTGTCCTCCAGCGCCTACCTG ICATGGAAGACTCACTAGTAATATGGTCTGCAAACACTGTGAACACCAGAGTCCTGTTCGATTTGATACCTTTGA1 CCTACAGCGGCTGAGCTGGTCCAGCCACGGCACGCCTCTGAAGCGGCATGAGCACGTGCAGTTCAATGAGTTC CATGCACTCTGGACACTTTGTCACTTACCGACGGTCCCCACCTTCTGCCAGGAACCCTCTCTCAACTAGCAATCA <u> GAACACCTGCTTCATGAACTCCCTGCTACAAGGCCTGTCTGCCTGTCCTGCTTTCATCAGGTGGCTGGAAGAGT</u> SAAAGCCTTGTCCTGCCAAGAAGTTACTGATGATGAGGTCTTAGATGCAAGCTGCTTGTTGGATGTCTTAAGAAT CCAGGGCCTACACTGGAGCTGCAGGATGGGCCGGGAGCCCCCACACCAGGTTCTGAATCAGCCAGGGGCCCCC AAAACACAGATTTTTATGAATGGCGCCTGCTCCCCATCTTTATTGCCAACGCTGTCAGCGCCGATGCCCTTCCCT TCCCAAACAAATTACCTGCCGCACAAGAGGGTCACCTCACCCCACATCCAATCACTGGAAGTCTCAACATCCTT CTCCCAGTTGTTCCCGACTACAGCTCCTCCACATACCTCTTCCGGCTGATGGCAGTTGTCGTCCACCATGGAGA CACCTCCCAGTACTCCAGGGATCAGAAGGAGCCCCCCTCACACCAGTATTTATCCTTAACACTCTTGCACCTTC CTGTTCTACGAGCGCGTCCTTTCCAGGATGCAGCACCAGAGCCAGGAGTGCAAGTCTGAAGAATGA

CCAGCCGGGACACTGTGATGGCGACGGTGAGGGGGGGCTTCGCCTGCGCCCCGGGCCCAGTTCCAGCGGCCCC CGAGCAGCTGGCGCGCTGGTGCGCGCGCTCTGGACTCGCGAATACACGCCCCAACTTTCCGCGGGAGTTCAAG AATGCAGTTTCCAAGTACGGCTCTCAGTTCCAAGGCAATTCCCAGCACGCCCTGGAATTCCTGCTCTGGTTG GCGCCGCCTGTTCAGCCGCTTCCTGCTGGCGCTGGGCAGCCGCTCACGCCCCGGGGACTCACCGCCCGGGC CGGGAGCCCCGGGGAGGAACGCCCGGCCCCGGACCCCAGCCCCAGCTCCAGCTCCCGCCGGCGATGGGGCGC GGCCGCCGGGCGCTCAGGGCTTGAAGAACCACGGCAACACCTGTTTCATGAACGCGGTGGTGCAGTGTCTCAG CTGGATCGTGTACATGAGGACCTGGAGGGTTCATCCCGAGGGCCGGTGTCGGAGAAGCTTCCGCCTGAAGCCA <u> AAGCACAATATAGATCTTCCTTGACTTGTCCCCACTGCCTGAAACAGAGCAACACCTTTGATCCTTTCCTGTGTGT</u> STCCCTACCTATCCCCTTGCGCCAGACGAGGTTCTTGAGTGTCACCTTGGTCTTCCCCTCTAAGAGCCAGCGGT >SGPR427_SEQID_18

 ICCTGCGGGTTGGCCTGGCCGTGCCGATCCTCAGCACAGTGGCAGCCCTGAGGAAGATGGTTGCAGAGGAGG
GGGAGCCTCCAGGAGGAGCGAGCGCAGGATGCCGACAGTGTGTGGCAGCAGCAGCAGCAGGCGCATCAGCAGCAC AAGAAGGAGAACAGGAGGAATGAGAGGGCAGAGGTCTCTCCACAGGTGCCCCCCGTCTCCCTGGTGAGTGGCG CTCCACAGAGGAGGAAGGTGCTAATCCTCTTCTGTAACTTGGTGGGGTCAGGGCAGCAGGCTAGCAGGTTTGG CAGGAGGCCAGGAGGCCCTCCACATGTCAAGCTGGCGGTGGAGTGGGATAGCTCTGTCAAGGAGCGCCTGTTC TGCCCCAGGTTCCTGACTCTCCCATCTTCACCAACAGCCTCTGCAATCAGGAAAAGGGGAGGGTTGGAGCCCAGG TTACGGCTCGGGAGCCACGCTGGCAGAGGGGAAGCCTGCTGTCCTGGAGCTCTGCCCCCTGCCCTCCC <u> ICTCAGCTCATCCACTGGGTCTGTCGGCCTCCCCACGCCTGGCAGCCCGTGAGGGCCAGCGATTCTCCCCTCTCT</u> GCCACCCTTCCTGATAAGGGAAGACAGAGCTGTTTCCTGGGCCCAGCTCCAGCAGTCTATCCTCAGCAAGGTCC AGCTGTACCTTGGATGATGTTTTCAGTTCTACACCAAGGAGGAGCAGCTGGCCCAGGATGACGCCTGGAAGTG TCCTCACTGCCAAGTCCTGCAGGGGATGGTGAAGCTGAGTTTGTGGACGCTGCCTGACATCCTCATCATCC ACCTCAAAAGGTTCTGCCAGGTGGGCGAGAGAAGAAACAAGCTCTCCACGCTGGTGAAGTTTCCGCTCTCTGGA CTCAACATGGCTCCCCATGTGGCCCCAGAGAAGCACCAGCCCTGAGGCAGGACTGGGCCCCTGGCCTTCCTGGA AGCAGCCGGACTGCCTGCCCACCAGTTACCCGCTGGACTTCCTGTACGACCTGTATGCCGTCTGCAACCACCAT GGCAACCTGCAAGGTGGGCATTACACAGCCTACTGCCGGAACTCTCTGGATGGCCAGTGGTACAGTTATGATGA CAGCACGGTGGAACCGCTTCGAGAAGATGAGGTCAACACCAGAGGGGGCTTATATCCTGTTCTATCAGAAGCGGA CATTCAAGACCATGCCTCTGCGGTGGTCCTTTGGATCCAAGGAGAAACCACCAGGTGCCTCCGTCGAGTTGGTG GTGAGGATGAGAAGTCAGCATCGCCGAGGTCCAACGTCGCCCTTCCTGCTAACAGCGAAGATGGTGGGGGGG ACAGCATCCCTCCCTGGTCAGCCAGCAGCTCCATGAGAGGCTCTACCAGCTCCTCCTCCTGTCTGATCACTGGCTC AAGGAGAGCTTCCAGATGGGAAGCAAAAGCAGCCCACCCTCCCCCTATATGGGATTCTCTGGAAACAGCAAAGA GCCTCTCACTGTGATGCCTTCAGTGGAGCATGAGAAACCAGCTCGACCGGAGGGCCAGAAGGCCATGAACTGG GTGGCCTGCAGCTATTTGTCTCCGAAGGACAGTCGGCCCCTCTGTCACTGGGCAGTTGACAGGGTTTTGCATCT GAGTACTTGGAATCCAGACGAAGACCTCGGTCCACGAGCCAGTCCATTGTGTCGCTGTTGACGGGCACTGCGG CATTGAAAGAGGTCCAGCCGGGGTGCCCTGTCCCTCGGCTCAACCCAACCACTGTCTGGCCCCTGGAAACTCA CAGTCGCCGAGGCACCTCTGAGCTAGACAGACCCCTGCAGGGGGACACTCACCCTTCTGAGGTCCGTGTTTCGG GECTGAGCCCTGCCATGGACGGGCAGGCTCCAGGCTCACCTCCTGCCCTCAGGATCCCAGAGGGCCTGGCCA SATGGTCCAAACACAGGAAGGAAACTCAAGGAAAATGCAGGGCAGGACATCAAGCTTCCCAGAAAGTTTGACCT GCCATCTTATGAAGAGTGAGGCCCCTGTACAGAACCTGGGGTCTCTGTTCTCCATCCGTGTTGTGGGACTCTCT SGGGCCTGGGCAGCCGGCTCGAGAGGGATGTCTGGTCAGCCCCCAGCTCTCCCGCCTCCCCCCTGTAAAGCCA GCAGGGCCCCGAGAGGCAGTGCACTGGGCATGTCACAAAGGACTGTTCCAGGGGAGCAGGCTTCTTATGGCAC

>SGPR092_SEQID_19

ATAATCTGTTCCTGGTTGCAACTCATGAGATTGGGCCATTCTTTGGGCCTGCAGCACTCTGGGAATCAGAGCTCCA FAATGTACCCCACTTACTGGTATCACGACCCTAGAACCTTCCAGCTCAGTGCCGATGATATCCAAAGGATCCAGC AATAAGCACACTCTAACTTACAGGATTATCAATTACCCACATGATATGAAGCCATCCGCAGTGAAAGACAGTATAT ITTTTACCAAATTCTGGAAATCCTGGAGTTGTCCATTTTGACAAGAATGAACACTGGTCAGCTTCAGACACTGGAT ATGCAGCTCGTCATCTTAAGAGTTACTATCTTCTTGCCCTGGTGTTTCGCCGTTCCAGTGCCCCCTGCTGCAGAC ATAATGCAGTTTCCATCTGGAGCAATGTGACCCCTTTGATATTCCAGCAAGTGCAGAATGGAGATGCAGACATCA <u> AGGTTTCTTTCTGGCAGTGGCCCCATGAAGATGGTTGGCCCTTTGATGGGCCAGGTGGTATCTTAGGCCATGCC</u> TCTGCTACACCAGCCCCACTGTGGGGTGCCTGATGGGTCCGACACCTCCATCTCGCCAGGAAGATGCAAGTGG CATAAAGGATGGGACTTTGTTGAGGGCTATTTCCATCAATTTTTCCTGACCAAGAAGGAGTCGCCACTCCTTACC ATTTGTATGGAGAAAAATGTTCATCTGACATACCTTAA

>SGPR359_SEQID_20

GTACAAGAATCCCTATGGATTCCACCTCCCCAAAGATGATGTGAAAGGGATCCAGGCATTATACGGACCTCGGAA AAATAAAGAAGGACACCAGATTGGTGAGATGGTTGCAAGAGGAAGCAATTCCATGATAAGGAAGATTAAGGAGCT FIGET CAT GAATT TIGG CCAT GCCCT GG CCCT GG CCCATT CCACAGACC CCAT CAGCACT GATG TACCCAACT TATAA SCTCATCCTTTGACGCTGTGACAATGCTGGGGAAGGAGCTCCTGCTCTTCAAGGACCGGATTTTCTGGAGACGG <u> ATGAAGGĪGCTCCCTGCATCTGGCCTTGCTGTCTTCCTCATGGCTTTGAAGTTTTCCACTGCAGCCCCTCC</u> GATCACGGGGATTCCTATCCATTCGATGGGCCTCGGGGGACTCTAGCCCATGCATTTGCTCCTGGAGAGGCCT GGGAGGAGATACACATTTCGACAATCCTGAGAAGTGGACTATGGGAACGAATGGTTTTAATTTGTTTACCGTTGC CTAGTTGCAGCCTCCCCCAGGACCTGGAGGAACAACTACCGCCTCGCACAGGCGTATCTTGACAAATATTACAC GAATATCTAAATACACACCTTCCATGAGTTCTGTCGAGGTGGACAAAGCAGTGGAGATGGCCTTGCAGGCCTGG AGTAGCGCCGTCCCTCTGAGCTTTGTCAGAATAAACTCAGGAGAGGGGGATATTATGATATCTTTTGAAAATGGA CAGGTTCACTTGCGGACAGGAATTCGGCCCAGCACTATTACCAGCTCCTTCCCCCAGCTCATGTGGGA TGCAGCTTACGAAGTGGCTGAGAGGGGCCACTGCTTACTTCTTCAAAGGTCCCCACTACTGGATAACAAGAGGAT ACAAGCGTTCTTTGGCCTCCAAGTCACCGGGAAGTTAGACCAGACCACAATGAACGTGATCAAGAAGCCTCGCT

U

-ccaaatgcaaggtcctcctcggactatttatgactttggatttccaaggcacgtgcagcaaatagatgctgctg ICTACCTCAGGGAGCCACAGAAGACCCTTTTCTTTGTGGGAGATGAATACTACAGCTACGACGAAAAGGAAAAGG AAAATGGAAAAAGACTATCCAAAGAATACTGAAGAAGAATTTTCAGGAGTAAATGGCCAAATCGATGCTGCTGTA

<u> ATGAACGTCGCGCTGCAGGAGCTGGGAGCTGGCAGCAACATGGTGGAGTACAAACGGGCCACGCTTCGGGATG</u>

SGPR104 1 SEQID 21

& A GAC GCACC C GAGAC C C C C G TAGA G G G G G G C C T C C C C G G C C C T G G A G G G G G T T C C A G A G G G

STGTGGTGAAATCTAGTTCCTGGATTGGTTGCTAA

FIG. 1X STGAACTTCGGTGGCATCGGTGTGGTCATGGGCCATGAGTTGACGCATGCCTTTGATGACCAAGGGGCGCGAGTA <u> S<u>G</u>CTTGAGTTCCTGTCTTTCTTGCTGTCACCATTGGAGTTGAGTGACTCTGAGCCTGTGGTGGTGTATGGGATGG</u> SGGGTCCCTCTTCGTGAAGGCCACGTTTGACCGGCAAAGCAAAGAAATTGCAGAGGGGGTGATCAGCGAAATCC <u> CACGAGGGAGCAGATGCAGCAGGTGCTGGAGTTGGAGATACAGCTGGCCAACATCACAGTGCCCCAGGACCAG</u> **ATTATTTGCAGCAGGTGTCAGAGCTCATCAACCGCACGGAACCAAGCATCCTGAACAATTACCTGATCTGGAACC** CAACTAAGAATGAGATCGTCTTCCCCGCTGGCATCCTGCAGGCCCCCTTCTATGCCCGCAACCACCCCAAGGCC FGGTGCAAAAGACAACCTCAAGCCTGGACCGACGCTTTGAGTCTGCACAAGAGAAGCTGCTGGAGAGCCTCTAT <u> ACAGCAATGTTATCCAGGTGGACCAGTCTGGGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCA</u> CGGCGCGACGAGGAGAAGATCTACCACAAGATGAGCATTTCGGAGCTGCAGGCTCTGGCGCCCTCCATGGACT SAAGGCAGTAGCAGGGACCTACAGGGCCACCCCATTCTTCACCGTCTACATCAGTGCTGACTCTAAGAGTTCCA AGCAGATGCCATCTATGATATGATTGGTTTCCCAGACTTTATCCTGGAGCCCAAAGAGCTTGGATGATGTTATGA GTTCTCCTGTGGGGGCTGGATTCGGAGGAACCCCCTGCCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGC SCAGAAGACACAGGGGTTCTACCTATCTTGCCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCCAGCCACTG SACCAGCTCCGCAAGCCTCCCAGCCGAGACCAGTGGAGCATGACCCCCCAGACAGTGAATGCCTACTACCTTC 4GAGACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAGGACAACTTTATGGAGGTGTT SCTGCATTCGAGTGGCTGGAAAAATCCTGGAGTCCCTGGACCGAGGGGTGAGCCCCTGTGAGGACTTTTACCA CGGGTACGAAATTTCTGAAGATTCTTCTTCCAAAACATGTTGAATTTGTACAACTTCTCTGCCAAGGTTATGGCT <u> GGCACTAAGAAGTCCTGTGTGCCGAGGTGGCAGACCTGCATCTCCAACACGGATGACGCCCTTGGCTTTGCTT</u>

ACTCTCTCCAACTCCCGTGACTTCCTGCGGCACTTCGGCTGCCCTGTCGGCTCCCCCATGAACCCAGGGCAGCT TGACAAAGAAGGGAACCTGCGGCCCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACCACACGGCCTGC ATGGAGGAACAGTACAATCAATACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACA TTGCTGACAACGGGGGGTGAAGGCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATGGGGAGGAGCA SCAACTGCCAGCCGTGGGGCTCACCAACCAGCTCTTCTTCGTGGGATTTGCCCAGGTGTGGTGTGCTCGGTC GTGTGAGGTGTGGTAG

>SGPR303 SEQID 22

CTGGGACCTTGTTACTTATAGGGAGACTGCATTGCTTATTGATCCAAAAAATTCCTGTTCTTCATCCCGCCAGTGG GGATTTAACTATCAGAATGAAGATGAAAAAGTCACCTTGTCTTTCCCTAGTACTCTGCAAACAGGTACGGGAACCT <u> GGACTCAGTTTGTTTCTGCTGATTACACCCGTGCCCAGGAGCTTGACGCCTTAGATAACAGCCATCCTATTGAAG</u> TGTGATGAATTGTGCTGATATTGATATTACAGCTTCATATGCACCAGAAGGAGATGAAGAAATACATGCTACA AGAGGTGCGCTATGCTGCTGTAACACAGTTTGAGGCTACTGATGCCCGAAGGGCTTTTCCTTGCTGGGATGAGC ACTCCTGTTGGCAAAGCAGAACAAGGAAAATTTGCATTAGAGGTTGCTGCTAAAACCTTGCCTTTTTATAACGACT GTGCTATCAAAGCAACTTTTGATATCTCATTGGTTGTTCCTAAAGACAGAGTAGCTTTATCAAACATGAATGTAATT <u> ACTTCAATGTTCCTTATCCTCTACCTAAAATTGATCTCATTGCTATTGCAGACTTTGCAGCTGGTGCCATGGAGAA</u> GACCGGAAACCATACCCTGATGATGAAAATTTAGTGGAAGTGAAGTTTGCCCGCACACCTGTTACATCTACATAT GTTGCTCTGGTTGTGGGACATGAACTTGCCCATCAATGGTTTGGAAATCTTGTTACTATGGAATGGTGGACTCAT TCAGTGTGGGCCATCCATCTGAGGTTGATGAGATATTTGATGCTATATCATATAGCAAAGGTGCATCTGTCATCC <u> ATGCCGGÁGAAGÁGGCCCTTCGAGCGGCTGCCTGCCGATGTCTCCCCCATCAACTGCAGCCTTTGCCTCAAGC</u> CTTTGGTTAAATGAAGGTTTTGCATCCTGGATTGAATATCTGTGTGTAGACCACTGCTTCCCAGAGTATGATATT

FIG.

1Y

>SGPR402_1_SEQID_23

GTCGAGCGCCTGGCACGCAAATTCGGCTTCGTCAACCTGGGGCCGATCTTCCCTGACGGGCAGTACTTTCACCT GGGTGGGCCCCGGTCCGAGCCCCCATCTATGTCAGCAGCTGGGCCGTCCAGGTGTCCCAGGGTAACCGGGAG SCGGCACCGGGGCGTGGTCCAGCAGTCCCTGACCCCGCACTGGGGCCCACCACCTGCACCTGAAGAAAACCC ATGCGGCCCGGATTGCGCTGTGGCTTGCGCTTGCCCTTGTTGGCCCTTGCCCTTGTCCGCCCCGGGCTGTG

AACAGCATCCACACGCTTTCCGTGGGCAGCACCACCCAGGAGGGCCGCGTGCCCTGGTACAGCGAAGCCTGC GCTACAACAACTGGGTCTTCATGTCCACCCACTTCTGGGATGAGAACCCACAGGGCGTGTGGACCCTGGGCCTA GGGCACGCTCTTCATCTGGGCCTCGGGCAACGGCGGCCTGCACTACGACAACTGCAACTGCGACGGCTACACC CACGGTGGACGGCCCCGGCATCCTCACCCGCGAGGCCTTCCGGCGTGGTGTGACCAAGGGCCGCGGGGCT GCAGGCCGAGGACTGGAGGACCAACGGCGTGGGGCGCCCAAGTGAGCCATCACTACGGATACGGGCTGCTGGA SCACACAGGGTGGTGACCGCTGGGCCTGGGCACACGGCGCGCCCCGCGCTGAGGGTCTGCTCCAGCTGCCC TGCCTCCTGCTACACCTGCCGCGGCGGCTCCCCGAGGGACTGCACCTCCTGTCCCCCATCCTCCACGCTGGAC TGGGGGTCGCTTTCAACGCCCGAATCGGAGGCGTACGGATGCTGGACGGTACCATCACCGATGTCATCGAGGC CCTCCACCCTCACCACCTACAGCAGCGGCGTGGCCACCGACCCCCAGATCGTCACCACGGGCCTGCATCA CCAGAGCCGCCCCACCCCATCCTGCCGCTGATCTACATCAGGGAAAACGTATCGGCCTGCGCCGGCCTCCAC GCAAAGAGACCGGCACGGGACCCGCTGTGCTGGGGAGGTGGCCGCGATGGCCAACAATGGCTTCTGTGGTG ATCTCGCTCACCAGCCCCATGGGCACGCGCTCCACACTCGTGGCCATACGACCCTTGGACGTCAGCACTGAAG ACATGACAGCGCGCCTACAGGCCCCCCAGGTGACCAGCAGCGCGTGTGTGCAGCGGGGACACAGAGGGGGCTGT CAGCAGCAGGGCTCCTGCATGGGACCCACCACCCCGGCAGAGCCGCCCCGGCTTAGAGCTGCCGCCTGTCCC CTGGTTCTCCAAGCAGTGGTACATGAACAGCGAGGCCCAACCAGACCTGAGCATCCTGCAGGCCTGGAGTCAG CCAGTCGCTGAGCCTGCAGCCGCAGCACATCCACATTTACAGCGCCCAGCTGGGGTCCCGAGGACGACGGCCG AACTCCATCCGCTCGCTGGAGCACGTGCAGGCGCAGCTGACGCTGTCCTACAGCCGGCGCGGGAGACCTGGAG GAGAACAAGGGCTACTATTTCAACACGGGGACGTTGTACCGCTACACGCTGCTGCTATGGGACGGCCGAGG CAAGGTGCAGTGGTTCCAGCAGCAGACGCTGCAGCGGGGGGGTGAAACGCTCTGTCGTGGTGCCCACGGACCC CACCACCECTECCCAGCCTCGGCCATGGTGCTGAGCCTCCTGGCCGTGACCCTCGGAGGCCCCGTCTTGC GGGCTGTCAGGCCAGGGCATCGTGGTCTGTGCTGGACGATGGCATCGAGAAGGACCACCCGGACCTCTGG GCCAACTACGACCCCCTGGCCAGCTATGACTTCAATGACTACGACCCGGACCCCCAGCCCCGGTACACCCCCA <u> GECATETCCATGGACCTCCCACTATACGCCTGGCTCTCCCGTGCCAGGGCCACCCCCACCAAACCCCAGGTCT</u>

1Z

FIG.

>SGPR434 SEQID 24

<u> GGCCCGGGCAGGCAGGGTGCGCAGGGAGGCGTAGCACTGCTCTTCCCCTCCGCGCTCCCCTCAGGGCC</u> A GGCGGCCAGGACCCCGGAGCGAGCGGATGGGAGCCGCCACCTGTAGGGGCTCCAGGATCCCCAGCGGCCC TTGGGTGACTGGCTGGAGCCAGGTTAAGCAGCGCTTTTCAGGCTCCACAGCCAACTCCATGCTGACCCCAGAGC STCACCTTCAGTGAGTACGTGCAGCCCATCTGCCTCCCGGAGCCCAATTTCAACCTGAAGGTTGGGACGCAGTG GTGTGGAGGGGCCCTCATTGACCCCAGCTGGGTGGTGACTGCGGCCCACTGCAGGCCAAGGCACAAAGATA ATCATTATGCACCCCAAGTACTGGGGCCGGGCCTTCATCATGGGTGACGTTGCCCTTGTCCACCTTCAAACACC <u> AGCCTTCTCAGGTCCCTGTGCCTCTGCCTGCTCCTGTTCCTGTGCTGGCCGCTGCAGCCCCAGATGGGCTCCT</u> CCCAGTCCAGGGGGAACGCAGTGCGCCCCGCTTCGGTGTTACTTCCCTCAGCCTGTGGCCAGCGGACTTCAAG TGGTGGTCGGAGGATTTGGAAATGACCCGCCATTGGCCCTGGGAGGTGAGCCTCCGGATGGAAAATGAGCACG ATCTGCGGAGGCTCCCTTATCGCCAGACACTGGGTTATAAAGAGGACACAACCAATCCAGTTTGTGGTGAGCCC CTCAGTGGTGCTTGGCACCTCCAAGCTGCAGCCCATGAACTTCAGCAGGGCCCTCTGGGTCCCTGTGAGGGAC GCAGGAGGCTGAGGTGTTTATCATGGACAACAAGAGGTGTGACCGGCATTACAAGAAGTCCTTCTTCCCCCCA GTTGTCCCCCTTGTCCTGGGGGGACATGATCTGTGCCACCAATTATGGGGAAAACTTGTGCTATGGGGATTCTGG AAGGCACAGAATCCAGGTGTGTACACCCGCATCACCAAATACACCAAATGGATCAAGAAGCAAATGAGCAATGG

>SGPR446 1 SEQID 25

CTGACGGCAGGCCACTGCATTTCCAGCCGTTTCCATTACAGTGTCAAGATGGGAGATCGGAGTGTCTATAATGAA TTGCATCAGAAATTCTTCAGGATGTGGACCAATACATGTGTGTTTGAGGAATGTAATAAGATAATACAGAAGGC CTTGTCATCTACTAAGGATGTAATAATAAAAGGGATGGTCTGTGGCTATAAAGAACAAGGAAAGGATTCTTGTCAA CCCTGGCAGGTGAGCGTGAGGACCAAAGGCAGGCACATCTGCGGCGCGCACCCTGGTCACCGCCACGTGGGTG AATTTCCAGGTGGAAGGTAGGACCAGGTGCTGGGTGACCGGATGGGGCAAAACACCCAGAACGTGGAGAAAAC SGAGATTCTGGGGGCCGCTTGGCCTGTGAATATAATGACACATGGGTCCAGGTAGGGATTGTGAGCTGGGGCA <u> ATCCTCACCCCAGTGTGTGGCCGAACCCCTCTGAGAATCGTGGGAGGAGGAGGCGCGGAGGAAGGGAGGTGG</u> GACCTTGCCCTTCTCCAGCTCCAACATCCTGTGAATTTTACCTCAAACATCCAGCCTATCTGCATCCTCAGGAG AACACAAGTGTGGGTCTCAGTCCAAAGAGCTTTTGTCCACCCTAAGTTCTCAACAGTTACAACCATTCGAAAT rcgectgtggtcgc

SGPR447_SEQID_26

SCAGCCTGCGCCTGAGGAGGCGCCACCGATGTGGAGGGAGCCTGCTCAGCCGCCGCCGCTGGGTGCTCTCGGCTG ATGGGCGCGCGCGGGGCGCTGCTGCTGCTGCTGCTGGCTCGGGCTGGACTCGGGAAGCCGGAGGCCTG

TCCGGAGGGTGATGTCCCACAGTACACCCAGGCCAAACCCCTCCCAGGTGTTGCTGCTCCTTGCCCTGCTGTGG CTGTTTGAACAGCCCTCTAGCCGTAGTATGATCTGGGATTCCATGTTTTGTGCTGGTGCTGAGGATGGCAGTGT SAGCTGGGGAATGGACTGCGGTCAACCCAATCGGCCTGGTGTCTACACCAACATCAGTGTGTACTTCCACTGGA <u> SGCACACCTCTGCCACCTCCTTACAACCTCCGGGAAGCACAGGTCACCATCTTAAACAACACCAGGTGTAATTAC</u> CCTTGGAACCTGCGGGCCTACAGCAGTCGTTACAAAGTGCAGGACATCATTGTGAACCCTGACGCACTTGGGGT CGCACTGCTTCCAAAAGCACTACTATCCCTCCGAGTGGACGGTCCAGCTGGGCGAGCTGACTTCCAGGCCAACT SACACCTGCAAAGGTGACTCAGGTGGACCCTTGGTCTGTGACAAGGATGGACTGTGGTATCAGGTTGGAATCGT ITTACGCAATGACATTGCCCTGCTGAGACTGGCCTCTTCTGTCACCTACAATGCGTACATCCAGCCCATTTGCAT SGAGTCTTCCACCTTCAACTTCGTGCACCGGCCGGACTGCTGGGTGACCGGCTGGGGGTTAATCAGCCCCAGT SCTCCC

SGPR432 1 SEQID 27

CCTGGCTGCAGGCTCGAGTTCAGGGGGCCAGCTTTCCTGGCCCAGAGCCCCAGAGACCCCGGAGATGAGTGATGA <u> ATCAGCTGTTCGCGCGTCTTCTCCTCCAGGTGGGGCAGGGGGTTTCGGGCTGGTGGAGCATGTGCTGGGACAGG</u> SCTGCCCACTGCTTCATTGGGCGCCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAGACCGGAGGAG A CAGCAT CCT CAAT CAAT CCAACAGCATATT CGGTT GCAT CTT CTACACACTACAGCTATTGTT AGGT CTT CAAGC SCTGCACCAGCGACACCTGTCCAACCCGGCCCGGCCTGGGATGCTATGTGGGGGCCCCCAGCCTGGGGTGCA FIGE TE GENERAL GENERAL DE LA GENERA DE LA COMPANTA DEL COMPANTA DE LA COMPANTA DEL COMPANTA DE LA COMPANTA DE LA COMPANTA DEL COMPANTA DEL COMPANTA DEL COMPANTA DE LA COMPANTA DEL COMP SECTCAGCETECCTGTGGACAGCGTGGCCCCCGGCCCCCCAAGCCTCAGGAGGGCAACACACAGTCCCTGGCGA STGGCCCTGGCAGGCCAGTGTGAGGAGGCAAGGAGCCCACATCTGCAGCGGCTCCCTGGTGGCAGACACCTG CTCTGCAGCGTGAGGGACTCAGCCCTGGGGCCGAAGAGGTGGGGGGTGGCTGCCCTGCAGTTGCCCAGGGCCT SGCCCCTGTCAGGGAGATTCCGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGACACTGGGTTCAGGCTGG <u> GAGGCCAGGCTGATGCACCAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTCAGAGGAGGCGGTGCTAACT</u> <u> ACGCGCTGCACGTGAAGGCGGCGCGCGCCCGGGACCGGGATTACCGCGCGCTCTGCGACGTGGGCACCGCC</u> SATECTCCTGGGACCCTACGCAATCTGCGCCTGCGTCTCATCAGTCGCCCCACATGTAACTGTATCTACAACCA SGTCCTCACTGCTGCCCACTGCTTTGAAAAGGCAGCAGCAACAGAACTGAATTCCTGGTCAGTGGTCCTGGGT SATCATCAGCTTTGCATCAAGCTGTGCCCAGGAGGACGCTCCTGTGCTGCTGACCAACACAGGTGCTGACAGTT

FIG. 1BB

CCGGCGGTCTTCACCGCGCTCCCTGCCTATGAGGACTGGGTCAGCAGTTTGGACTGGCAGGTCTACTTCGCCG CCGGGGGATGGTGTGTACCAGTGCTGTGGGTGAGCTGCCCAGCTGTGAGGGCCCTGTCTGGGGCCACCACTGGTG CATGAGGTGAGGGGCACATGGTTCCTGGCCGGGCTGCACAGCTTCGGAGATGCTTGCCAAGGCCCCGCCAGG

>SGPR529 SEQID 28

36GATGACCACCTGCTGCTTCTTCAGGGCGAGCAGCTCCGCCGGACGACTCGCTCTGTTGTCCATCCCAAGTAC ATGAGAGCTCCGCACCTCCACCTCTCCGCCGCCTCTGGCGCCCGGGCTCTGGCGAAGCTGCTGCCGCTGCTGCTGCT <u> AGGTTGCTGGCTGGGGCACCACGGCCGCCCGGAGAGTGAAGTACAACAAGGGCCTGACCTGCTCCAGCATCAC</u> CACCAGGGCTCAGGCCCCATCCTGCCAAGGCGAACGGATGAGCACGATCTCATGTTGCTAAAGCTGGCCAGGC ACCGGGGCCAGGACCCTTGCCAGAGTGACTCTGGAGGCCCCCTGGTCTGTGACGAGGCCCTCCAAGGCATCCT SCGTAGTGCCGGGGCCCCGCGTCCGGGCCCTGCAGCTTCCCTACCGCTGTGCTCAGCCCGGAGACCAGTGCC TGGCGCAACTCTGGGCCGCAGAGGCGGCGCTGCTCCCCCAAAACGACACGCGCTTGGACCCCGAAGCCTATG SCGCCCCGTGCGCGCGCGCGCAGCCCTGGCAGGTCTCGCTCTTCAACGGCCTCTCGTTCCACTGCGCGG ATCCTGAGCCCTAAAGAGTGTGAGGTCTTCTACCCTGGCGTGGTCACCAACACAACATGATATGTGCTGGACTGG GTGTCCTGGTGGACCAGAGTTGGGTGCTGACGGCCGCGCACTGCGGAAACAAGCCACTGTGGGCTCGAGTAG STCGTGGGGTGTTTACCCCTGTGGCTCTGCCCAGCATCCAGCTGTCTACACCCAGATCTGCAAATACATGTCCT **3GATCAATAAAGTCATACGCTCCAACTGA**

FIG. 1CC

SGPR428_1_SEQID_29

SGTCATGGGAACGAGAACATTCAGCAACATCCACTCGGAGAGAAAGCAAGTGCAGAAGGTCATTATTCACAAATA STGGGGTGTGGGCTGTGGCCAGAAGAACATGCCTGGAGTGTACACCGAGTTGTCCAATTATCTGCTTTGGATCG **AAAACGTACAATGTGGCCACAGGCCTGCTTTTCCAAACTCGTCATGGTTACCATTTCATGAACGGCTTCAAGTCC** TACAAACCGCCCCAGCTCGACAGTGACCTCTCTCTGCTTCTACTTGCCACCACCAGTGCAATTCAGCAATTTCAA AATGCCTGTCTGCCTGCAGGAGGAGGAGAGGACCTGGGACTGGTGTTGGATGGCACAGTGGGTAACGACAAT SGGTATGACCAATATGATGACTTAAACATGCACCTGGAAAAGCTGAGAGTGGTGCAGATTAGCCGGAAAGAATG <u> AGAATGGTGAGTGCCCGTGGCAAGTGAGTATCCAGATGTCACGGAAACACCTCTGTGGAGGCTCAATCTTACAT</u> GGTGGTGGGTTCTGACAGCCGCACACTGCTTCCGAAGAACCCTATTAGACATGGCCGTGGTAAATGTCACTGT

AGAGGAAGACTGTGCTGGCAGGGAAGCCGTATAAGTATGAGCCAGACTCTGTGTACGCTTTGCTTCTCTCACCC TGGGCCATCCTGTTACTGTATTTTGTGATGCTTCTATTATCCT

>SGPR425 SEQID 30

GACTATGTCAAAGGGAGTAAAAAGCTAAGGGTAGGGTTGTTGAAGATGAGGAATAAAAGTGGAGGCAAGAACG 3AGAGAGCGAAGGGTGGGAGAAGAAGAAAAAATCTGGCCGGGGTCAGAGGATTGCCGAAGGGAGGCCTTCCT GTTTTGCAGTGTGTCCGACGAATCCAATGATCTCCTTTACCAATACTGCGATGCTGAGTCGGGCTCCACCGGTTC rccacgggctgtagtggcattctcatttcccctcagcatgttctaactgctgcccactgtgttcatgatggaaag <u>GATCAAGAAAATGCCTGGTGGAATGATCCACTTCTCAGGATTTGATAACGATAGGGCTGATCAGTTGGTCTATCG</u> TTCTGAATTGGAGGATTATCTTTCCTATGAGACTGTCTTTGAGAATGGCACCCGAACCTTAACCAGGGTGAAAGT **GGGGTCTATCTGCGTCTGAAAGATCCAGACAAAAGAATTGGAAGCGCAAAATCATTGCGGTCTACTCAGGGC** <u> ACCAGTGGGTGGATGTCCACGGGGTTCAGAAGGACTACAACGTTGCTGTTCGCATCACTCCCCTAAAATACGCC</u> <u> SAAGATTTGGTTCTTGAGCCGACTCAAAATATCACCACAAAGGGAGTATCTGTTAGGAGAAAGAGACAGGTGTAT</u> ATGGAAAATATGCTGCTTTGGTTGATATTTTTCACCCCTGGGTGGACCCTCATTGATGGATCTGAAATGGAATGG TTCAGTGGACCCGGGTCAAGAATACCCACATTCCGAAGGGCTGGGCACGAGGAGGCATGGGGGACGCTACCT GGCACCGACAGCAGGTTCAGCATCTTGGACAAAAGGTTCTTAACCAATTTCCCTTTCAGCACAGCTGTGAAGCT GATTTTATGTGGCACTTGAGAAAGGTACCCCGGATTGTCAGTGAAAGGACTTTCCATCTCACCAGCCCCGCATT CAGATTTGCCTCTGGATTCACGGGAACGATGCCAATTGTGCTTACGGCTAA

FIG. 1DD

>SGPR548 SEQID 31

TGTTGCTGCGCCTAGTCCAGCCCGCACGCCTGAACCCCCAGGTGCGCCCCCGCGGTGCTACCCACGCGTTGCCC <u> CCACCCGGGGGGGGCCTGTGTGTGTCTGGCTGGGCCTGGTGTCCCACAACGAGCCTGGGACCGCTGGGAG</u> <u> ATGGGGGACCCAGAAGGAAGCGCAGAGTGGGGTTGGGGGAAGGGGATACCGGTGGTCAGAAGAAATTTATTAA</u> CAGTGGATGGGATAAGTCTGTGTCTGGAGGGATCCTGGTGGAGGCCAGAAGGGTCCTGCCTCACCTGGATTCTC1 GGCAAGTGGCTCTCTACGAGCGTGGACGCTTTAACTGTGGCGCTTCCCTCATCTCCCCACACTGGGTGCTGTCT GCGGCCCACTGCCAAAGCCGCTTCATGAGAGTGCGCCTGGGAGAGCACAACCTGCGCAAGCGCGATGGCCCA CTGGCATCCACAGCAGCCCAGGATGGTGACAAGTTGCTGGAAGGTGACGAGTGTGCACCCCCACTCCCAGCCAT

CCCCCGGTCACAAGTGAGTCTCCCAGATACGTTGCATTGTGCCAACATCAGCATTATCTCGGACACATCTTGTGA TGAGGGTGACTCTGGGGGACCCCTGGTCTGTGGGGGCATCCTGCAGGGCATTGTGTCCTGGGGGTGACGTCCCT TGTGACACACCCACCAGCCTGGTGTCTATACCAAAGTCTGCCACTACTTGGAGTGGATCAGGGAAACCATGAA GAGGAACTGA

>SGPR396 SEQID 32

CACCTTCACTTCTGCCATCCTGCCTATTTGCTTGCCCAGTGTCACAAAGCAGTTGGCAATTCCACCCTTTTGTTGG <u> ATGGGCCCTGCTGCCTGCCTTCACGCTGCTCCTTCTGCTGGGGATCTCAGTGTGTGGGGAACCTGTATACTC</u> CAGCCGCGTTGTAGGTGGCCAGGATGCTGCTGCAGGGCGCTGGCCTTGGCAGGTCAGCCTACACTTTGACCAC TGTCGTGTCACATTGATGGTGTATGGATCCAGACAGGAGTAGTAAGCTGGGGGATTAGAATGTGGTAAATCTCTTC CATTATTGACCGCCAGGCTTGTGAACAGCTCTACAATCCCATCGGTATCTTCTTGCCAGCACTGGAGCCAGTCAT STCTGACTTCTTGTTCCCTATTGTCCTACTCTCTCTGGCTCTCCTGCGTCCCTCCTGTGCCTTTGGACCTAACACT GTCCAAAATCGTCATCCATCCCAAGTACCAAGATACAACGGCAGACGTCGCCTTGTTGAAACTGTCCTCTCAAGT GTGACCGGATGGGGAAAAGTTAAGGAAAGTTCAGATAGAGATTACCATTCTGCCCTTCAGGAAGCAGAAGTACC CAAGGAAGACAAGATTTGTGCTGGTGATACTCAAAACATGAAGGATAGTTGCAAGGGTGATTCTGGAGGGCCTC AACTITATCTGTGGAGGTTCCCTCGTCAGTGAGAGGTTGATACTGACAGCAGCACACTGCATACAACCGACCTG GACTACTTTTCATATACTGTGTGGCTAGGATCGATTACAGTAGGTGACTCAAGGAAACGTGTGAAGTACTACGT CTGGAGTCTACACCAATGTAATCTACTACCAAAAATGGATTAATGCCACTATTTCAAGAGCCAACAATCTAGACT TCCCAGGGGCAGATAA

FIG. 1EE

>SGPR426 SEQID 33

STIGITGAGGATGATAAGTCTTTCTATTACCTTGCCTCTTTTAAAGTCACAAATATCAAATATAAAGAAAATTATGG TGAAGACCAAACAATTGTCTTTGACCATAAACAAACCATCATTTAGACTCACACGCTGTGGAATAAGGATGACAT ACTCAGTACGGCTAGCTCTTTTCACATTAGCAATTGTAGCAATCATAGGAATTGCAATTGGTATTGTTACTCATTT ICTGTAGGCGGTCGATTTATCAAATCTCATGTTATCAAATTAAGTCCAGATGAACAAGGTGTGTGGATATTCTTATAG CATAAGATCTTCAAGAGAGTTTATAGAAAGGAGTCATCAGATTGAAAGAATGATGTCTAGGATATTTCGACATTCT

TATAACACCACCGCAGTGAAACGAAATGTGAGGAAAATTATTCTTCATGAGAATTACCATAGAGAAACAAATGAA CATCTATAAAGTTGCCACCTAAAACAAGTGTGTTCGTCACAGGATTTGGATCCATTGTAGATGATGGACCTATACA &AATACACTTCGGCAAGCCAGAGTGGAAACCATAAGCACTGATGTGTGTAACAGAAAGGATGTGTATGATGGCCT **ICTGGTTTATGATAATCATGACATCTGGTACATTGTAGGTATAGTAAGTTGGGGACAATCATGTGCACTTCCCAAA** AATGACATTGCTTTGGTTCAGCTCTCTACTGGAGTTGAGTTTTCAAATATAGTCCAGAGAGTTTGCCTCCCAGACT A T G G C T G C T C A C T G C T T T T G G A A A A A A G A C C C A C T C A T G G A T T G C T A C T T T G G T G C <u> AAACCTGGAGTCTACACCAGAGTAACTAAGTATCGAGATTGGATTGCCTCAAAGACTGGTATGTAG</u>

>SGPR552_SEQID_34

AAGCATGTCTTCCAGATGTTAATTATATATTCCTATACAATTCAGAAGCAGTGGTTACTGCATGGGATCATTTAAA <u>AGAATAGCAGAGGGTCTGGATGCTGAGGAAGGAGTGGCCCTGGCAAGCTAGCCTTCCACAGAACAATGTCTA</u> CCAAAGAATGGAATGTTATTTTAAGTAACCCACAAACACAGTCAAATATCAAGAATGTTATAATTCAAGAAAACTAC <u> AGGGTGACTCTGGTGGACCACTGGTTGGTACAGATTCTAAAGGCATCCTTGCTAAAGGTTCCCTGCTGGTATTGA</u> CCGACGCGGAGCCACATGGCTTAGTAACAGCTGGCTTATCACTGCTGCTCACTGCTTCATAAGGGTCCATGATC CCTTTACGAACAACTTCTAATGTACTCCACAAGGGATTAGTGAAGATTATAGATAATAGGACCTGCAACAATGGG A A G C T G G A G T A A A T G A A C G T G C T T C C A A C A A G C C T A G T C T C A A G T G A C A T A C T A T

FIG. 1FF

>SGPR405_SEQID_35

CCCTCACAGGTCCGGGCAGCCTTCCTAGAGGAGGTGGCATTGAGGTGGGCATGGAGTTTCCGGGATGCAGCGG GACCCAAGCGACGGCAGCAGGGGTCAGCAGAGGGGCCTGCGGCGGGGGTGGACGCTGGAGCAGGAGACCAGG **ATGGTCAĞCAAGĞGGGGAGTTGCTGCAGAGCCAGAGCCACACTATTGTGAGGGACAGTGAAAGAGGGCCCCAACA** GTTTAGAGTGCAGGTGGGGCAGCTGAGGCTCTATGAGGACGACCAGCGGACGAAGGTGGTTGAGATCGTCCGT TCCCAATAGACAGCAAACACCTGAAACCGGTGATCAGCAGCTTCCCGGTAAGATCTCAGGAGCTGGGCCGAGGG CACCCCCAGTACAACGAGAGCCTGTCTGCCCAGGGCGGTGCGGACATCGCCCTGCTGAAGCTGGAGGCCCCG GGCTGGAGCAGGCACACTAAGAGGCAAAATGGCAGAGTTTAACTGGTCTATGGCCTTCAAGGGACCTGCGGCT GGTCATGAAGAGCGCCTCAACTCTGTGTCCAGCAGGGCCAAGAAGGGCCATTGGCTGGGATGTCGCTGCTGCTT

GCAGGTGAAGGTCCTCACACTGAGCAATGCAGACTGTGAGCGGCAGACCTACGATGCTTTTCCTGGTGCTGGAG CGGCCCAGCATTGGCGTCTACACACGCCCAGAGACCAGCTGGCAGGGTGCCAACCATGCAGACGCCCAGAGAC CCTGCTACCCAATGGCTGTCCCCAGCACCCTTACCCACGTCACCTGCCACCCGGCGGCCATCCCCAGGCCCTTC GCTGGGTGACCGGCTGGGGTGTCATTGGACGTGGAGAACTACTGCCCTGGCCCCTCAGCTTGTGGGAGGCGAC ACCCACATCACCTGCTACACGATGGCCATCCCCAGGCCTTCAACCACGCCACCTGCTACACGACGGCCATCCCC GTGGTCGTGGCAGTGGGTGCTGACCGCCGCTCACTGCATTTTCCGGAAGGACACCGACCCGTCCACCTACCGG CCCAGCACCCTCACCCACGTCACCTGCTACCCGACGGCCGTCCCCAGGCCCTTCACCCATGTCACCTGCTACCT <u> AGCACCCTCACCCACGTCACCTGCTACACGATGGCCGTCCCCAGGCCCATCACCCATGTCACCTGCTACACGAT</u> TCACCCACGTCACCTGCTACCCGACGGCCATCCCCAGGCCCTTCACCCATGTCACCTGCTACCTGATGGCTGTC GGGGCCCCCTCCTGTGCAGGCGGAATTGCACCTGGGTCCAGGTGGAGGTGGTGAGCTGGGGCAAACTCTGCG TGATGGGATCAGGAGCGCCGCTGCCCCGGCCCCCGACCTGCAAGAGGCCCGAGGTCCCCATCATGAGGACCC STGTGCAGGGAGGAAGGGGCAGGGTTCCTGCCAGGCCGCTCTGAGGACGGAGGACCTCACCCCAACCACACC STACTCTGTCTTCCTGGGGGCAGACATCGCCCTGCTGAAGCTGGCCACCAGTTCCCTGGAGTTCACTGACA CGGCCCCCTGGTCTGCAAGAAGAAGGGTACCTGGCTCCAGGCGGGAGTAGTGAGCTGGGGATTTTACAGTGAT <u>GATGGCTGTCCCCAGCACCCTCACCCACATCACCTGCTACATGATGGCCGTCCCCAGGCCCTTTACCCACATCA</u> GAGCTTGCGAGAGGATGTATCACAAAGGCCCCACTGCCCACGGCCAGGTCACCATCATCAAGGCTGCCATGCC <u> 2AGCTGGCAGGGTGCCAACCATGCAGAGGCCCAGAGACATGGGCCAGGGCCAGGAGTGGGTCTGCAGGCCCT</u> TTGAGCGGCTCATCAAGGACGACATGCTGTGTGCCGGGGACGGGAACCACGGCTCCTGGCCAGGCGACAACG AGCTCAGACCCCTGCTGTGGTCCGAAGATTTGTGCTCCCCCCCAAATCCAGATGTTGAAGCCCTAACTCCAGTG CAACACGGAGGTGTCTCCACGTGCAGACCCCAGGCTGAGCCAGGCGGAGGACATCTGGCCAGAGTGGGCTTG <u> ACTGGGAGTCCAGCTCCCGTCCCCGAGAATGACCTGGTGGGCATTGTGGGGGGCCACACACCCCCAGGGGAA</u> **ATTCACACCAGGGATGTGTATCTGTACGGGGCCGGGGGCTGCTGAATGTCAGCCAGATCGTCGTCGTCCACCCAA** GTGCCGCTGTCTGAGCTCATCCACCCGGTCTCGCTCCCGTCTGCCTCCCTGGACGTGCCCTCGGGGAAGACCT

A TECT CCT GTT CT CAGT GTT G CT G CT C CT G GT C A C G A G A A CT C A G CT C G G T C C A C G A CT C C T C C C

SGPR485 1 SEQID 36

FIG. 1HH

 4GGGTGACAGTGGGGGCCTCTGGTCTGCACCCCAGAGCCTGGTGAGAAGTGGTACCAGGTGGGCATCATCAG
<u> AACAAGTGGTGGATTCTCACTGCGGCTCACTGCTTATATTCCGAGGAGCTGTTTCCAGAAGAACTGAGTGTCGTG</u> STGGGGAAAGAGCTGTGGAGAGAAGAACACCCCAGGGATATACACCTCGTTGGTGAACTACAACCTCTGGATCG 26GAGGTGGGTGAGTTTCCGTGGCAGGTGAGTATTCAGGTAAGAAGTGAACCTTTCTGTGGCGGCTCCATCCTC AGAAAGTGACCCAGCTAGAGGGCAGGCCCTTCAATGCAGAGAAAAGGAGGACTTCTGTCAAACAGAAACCTATG SCCCATCTGCCTCCCCACGCAGCCCGGCCCTGCCACATGGCGCGAATGCTGGGTGGCAGGTTGGGGGCAGAC SECTCCCCAGTCTCGGGAGTCCCAGAGCCAGGCAGCCCCAGATCCTGGCTCCTGCTCTGTCCCGTGTCCATG CAATGCTGCTGACAAAACTCTGTGAAAACGGATCTGATGAAAGCGCCAATGGTCATCATGGACTGGGAGGAGT GTTCAAAGATGTTTCCAAAACTTACCAAAAATATGCTGTGTGCCGGATACAAGAATGAGAGCTATGATGCCTGCA 4GAGGCTGGAGTGGCTATCCTAGGCAGGGCTAGGGGAGCCCACCGCCCTCAGCCCCTCATCCCCCAGCCC AAGAGAGCCAACATGGACAATGACATTGCCTTGCTGCTGCTTCGCCCATCAAGCTCGATGACCTGAAGGT STGGGGACCAACGACTTAACTAGCCCATCCATGGAAATAAAGGAGGTCGCCAGCATCATTCTTCACAAAGACTT IGTTGTTCAGAGCTATTTTGTACTGA

>SGPR534 SEQID 37

ATCCAGGTCCTGAAGATCGCCAAGGTCTTCAAGAACCCCAAGTTCAGCATTCTGACCGTGAACAATGACATCACC <u>GACGTGATCTGTGCCGGGGCCAGTGGCGTCTCCTCCTGCATGGGTGACTCTGGAGGCCCCCTGGTCTGCC</u> ACTTCCCCGCGGGGACACTGTGTGCCACCACAGGCTGGGGCAAGACCAAGACGCCAACAAGACCCTGA SAAGCTGCAGCAGGCAGCCCTGCCCTCCTGTCCAATGCCGAATGCAAGAAGTCCTGGGGCAGGAGGATCACC GCCCACTGCGGGGTCAGGACCTCCGACGTGGTCGTGGCTGGGGAGTTTGACCAGGGCTCTGACGAGGAGAAC STCCCTGCAGGACAAAACCGGCTTCCACTTCTGCGGGGGCTCCCTCATCAGCGAGGACTGGGTGGTCACCGCT CCCTGTGCTCAGCGGCCTGTCCAGGATCGTGAATGGGGAGGACGCCGTCCCCGGCTCCTGGCCTGGCAGGT 4GAAGGACGGAGCCTGGACCCTGGTGGGCATTGTGTCCTGGGGCAGCCGCACCTGCTCTACCACCACGCCCG STGTGTACGCCCGTGTCACCAAGCTCATACCCTGGGTGCAGAAGATCCTGGCCGCCAACTGA

CACACCATCTTTAAGAAATGTAACACTCAGCCCTTCCTCTACACAGGGCTTCCACGTGGACCACACGGCCGAG SCTGCGGGAACAGCCAGTGTGTGACCAAGGTGAACCCGGAGTGTGACGACCAGGAGGACTGCTCCGATGGGTC SAGCCCTCTGGCCGGTTCTTTCTGGCTGGCATCGTGAGCTGGGGAATCGGGTGTGCGGAAGCCCGGCGTCCAG <u> AGCGAGGGATCCGGGCAAGGCTGCGGGAGCACGGCATCTCCCTGGCTGCCTATGGCACAATTGTGTCGGCTGA</u> CGACGAGGCGCACTGCGAGTGTGGCTTGCAGCCTGCCTGGAGGATGGCCGGCAGGATCGTGGGCGGCATGGA A T CAAC G C C A G G T G C T G C T G C T C C T T C A T G A G T T C C A G A C C C G A G A G T G G G T G G C C T SCCCACCATGGCTCCTGCCCCTGCCGCCCCCAGCACAGCCTGGCCCACCAGTCCTGAGAGCCCTGTGGTCAGC 4GCATCCCCGGGGGGGTTTCCGTGGCAAGCCAGCCTTCGAGAGAACAAGGAGCACTTCTGTGGGGGCCGCCATC SCTGGACTTCGACCTGGCTGTCCTGGAGCTGGCCAGCCCCTGGCCTTCAACAAATACATCCAGCCTGTCTGCC STGGAGGCACTGCTGCACTTTCTGCTGCGACCCCTCCAGACGCTGAGCCTGGGCCTGGAGGAGGAGGTATTGC SEGICTATECCCEAGICACCAGGCTACGIGACTGGATCCTGGAGGCCACCACCAAAGCCAGCATGCCTCTGGC GCCCCTGGCCATCCAGAAGTTCCCTGTGGGCCGGAAGTGCATGATCTCCGGATGGGGAAATACGCAGGAAGG **AAATGCCACCAAGCCCGAGCTCCTGCAGAAGGCGTCCGTGGGCATCATAGACCAGAAAACCTGTAGTGTGTCTCT** SAAGCAAGACCACGAACCCACCAGAAGGAAGAATTCCGAACACATCCGAACATCAGCAAGAACAACATCCGGA SETGGGTGCGACCTACCTCAGCGGCTCGGAGGCCAGCCGTGCGGGCCCAGGTGGTCCAGATCGTCAAGCA SCCCCTGTACAACGCGGACACGGCCGACTTTGACGTGGCTGTGCTGGAGCTGACCAGCCCTCTGCCTTTCGGC STGTGCGCTGGCTACCTGGACGGGAAGGTGGACTCCTGCCAGGGTGACTCAGGAGGACCCCTGGTCTGCGAG ACCCCCACCAAATCGATGCAGGCCCTCAGTACCGTGCCTCTTGACTGGGTCACCGTTCCTAAGCTACAAGAATG 36GCCTGGGCGGGAGCCCGGTGAAGATCGGGCTGCGGCGGGTAGTGCTGCACCCCCCTCTACAACCCTGGGCAT STGCGGGGAATCCGGTGGACCAGCAGTTTGCGGCGGGAGACCTCGGACTATCACCGCACGCTGACGCCCACC <u> 18 TCTGCCGCCCACTGCTTCAACCACACGAAGGTGGAGCAGGTTCGGGCCCCACCTGGGCACTGCGTCCCTCCT</u> SAAAGCCACTGTGGAGCTGCTGGACCAGGCACTGTGTGCCAGCTTGTACGGCCATTCACTGACAGGATG SCTGGGGCTACCTCAAGGAGGACTTCCGTAAGCATCTTCCTCGGCCTGCAATGGTCAAGCCAGAGGTGCTGCA <u> SCTCACAGGGAGACATAAGGGACCCTTGGCAGAAAGAGACTTCAAATCAGGCCGCTGTCCAGGGAACTCCTTT</u>

SCTGTCGAGCGGCCAGCATTGGCGTGGTGGCCACCAGCCTTGTCGTCCTCACCCTGGGAGTCCTTTTGGGAGG

<u> ATGGAGCCCACTGTGGCTGACGTACACCTCGTGCCCAGGACAACCAAGGAAGTCCCCGCTCTGGATGCCGCG</u>

>SGPR390 SEQID 38

4ATGAACAACTCCAGACACGCTGCCTTAAGAGCTGCAACACTCCCTGGGAAGGTCTACAGCGTCACTCCTGAAG

TCTGGGGGCCCCCTGGCGAGGAGGCCCCTGGCGTGTTTTATCTGGCAGGGATCGTGAGCTGGGGTTTT AGCGAGCAGACCTGCCGCCGCTTCTACCCAGTGCAGATCAGCAGCCGCATGCTGTGTGCCGGCTTCCCGCAGG ACAACTTCTCCCTCACAGACCGCATGATCTGCGCAGGCTTCCTGGAAGGCCAAAGTCGACTCCTGCCAGGGTGAC GCTGGCCTCACAGTCCCGGGGGCCACACCCCAGCAGCCCACCCTGGGGCTGCCAGCAGGGTGACGGGCCAA <u>CAGCGGCCCGTGGGGAGTGGCCGTGGCAGGTGAGCCTGTGGCTGCGGCGCCCGGGAACACCGTTGCGGGGCCC</u> GTGCTGGTGGCAGAGAGGTGGCTGCTGTCGGCGGCGCACTGCTTCGACGTCTACGGGGACCCCCAAGCAGTGG GTCCTCCCAGCCCCTTCCCATGTCTCCCCCCTCGACCACAAGGATGCTGGCCACCACCAGGCCCCAGGACGACA CCTGCCAACTCAACCTTATCTGCCGTGAGCACCACTGCTAGGGGACAGACGCCATTTCCAGACGCCCGGAGG CCGGCTGGGGCTCGGTGCGCGAAGGAGGCTCCATGGCGCGGCAGCTGCAGAAGGCGGCCGTGCGCCTCCTC SCTGCGCTCAGGTTAAGAAGCCGGGCGTGTACACGCGCATCACCAGGCTAAAGGGCCTGGATCCTGGAGATCA1 1GTGAGAGGCTGGATAGGACAGCACATCCAGGAGTGA

>SGPR521_SEQID_39

GGCTGTCATCCATGGTGAAGAAAGTCAGGCTGCCCTCCCGCTGCGAACCCCCTGGAACCACCTGTACTGTCTCC ATGAGTACACCGTGCACCTGGGCAGTGATACGCTGGGCGACAGGAGGGCTCAGAGGGATCAAGGCCTCGAAGTC GGCTGGGGCACTACCACGAGCCCAGATGTGACCTTTCCCTCTGACCTCATGTGCGTGGATGTCAAGCTCATCTC GGCAATCAGCTCCACTGCGGAGGCGTCCTGGTCAATGAGCGCTGGGTGCTCACTGCCGCCCACTGCAAGATGA CCCCCAGGACTGCACGAAGGTTTACAAGGACTTACTGGAAAATTCCATGCTGTGCGCTGGCATCCCCGACTCCA AGAAAAACGCCTGCAATGGTGACTCAGGGGGACCGTTGGTGTGCAGAGGTACCCTGCAAGGTCTGGTGTCCTG ATTCCGCCACCCGGCTACTCCACACACAGACCCATGTTAATGACCTCATGCTCGTGAAGCTCAATAGCCAGGCCA GGGAACTTTCCCTTGCGGCCAACCCAATGACCCAGGAGTCTACACTCAAGTGTGCAAGTTCACCAAGTGGATAA ATGGCAAGATCCCTTCTCCTGCCCCTGCAGATCCTACTGCTATCCTTAGCCTTGGAAACTGCAGGAGAAGA ATGACACCATGAAAAAGCATCGCTAA

>SGPR530 1 SEQID 40

GCCTGGGTCCTGGTGGGGCTGGCCAGCTGGGGCCTGGACTGCCGGCATCCTGCCTACCCCAGCATCTTCACCA SAAGACCATAAGAGGGTGCAACTGTCACCACCCTTCTATCTCCAGGAGGGCAAGGTGGGCCTCATTGAGAACAC GGGTCACCTACTTCATCAACTGGATTGACGAAATCATGAGGCTCACTCCTCTTTCTGACCCCGCGCTGGCTCCTC GGTATCAACTACCCACTGCTTTCTCAACAAATCCCAGGCCCCGAAGAACTATCAGGTTCTGTTGGGAAACATCCA GGGGGTACTTCTCGACAGGAAAGTCCATCTGCAAAGGCGATTCTGGGGGGCCTCTAGTCTGCTACCTCCCAGT <u> GTCTCCACAGTGTGTGGGAAGCCTAAGGTGGTGGGGAAGATCTATGGTGGCCGGGACGCAGCAGCTGGCCAGT</u> ACTGTATCATCAAACCCAGCACACCCAGAAGATGTCTGTGCACCGGATCATCACCCATCCAGACTTTGAGAAGCT ACTCTGTAATACCTTATATGGGCAAAGAACTGCAAAGGCGAGACCTAAGCTTTGCACGAGGAGATGCTGTGTG <u> CCACCCCTTTGGGAGTGACATTGCCATGTTGCAGCTGCACCTGCCTATGAACTTCACTTCCTACATTGTCCCTGT</u> CTGCCTCCCATCCCGGGACATGCAGCTGCCCAGTAACGTGTCCTGTTGGATAACCGGCTGGGGAATGCTCACC 36CCATGGCAGGCCAGCCTGCTCTACTGGGGCTCGCACCTCTGTGGAGCTGTCCTCATCGACTCCTGCTGGCT

>SGPR520 SEQID 41

1KK

ATECTECTGCTGCTGCTGCTGCTGCTACCCCTCCCAAGCTCATGGTTTGCCCCACGGGCACCCACTGTACACACG CCTGCCCCCCAGCGCCCTGCAAGTCTTCACTCTCCTTTGGGGGCCAGAGACTGTGTTGGGCCGCAACCTAGACT TGGGGGGCAGCGCGCGCCCCGGGGCCTGGCCCTGGCTGGTGAGGCTGCAGCTCGGCGGGGGGAGCTTTG CCTGCCGGAACCGCCTGCGCCATCGCGGGCTGGGGCCCCCTCTTCGAAGACGGGCCTGAGGCTGAAGCAGTG SCCCGGCTCTGCGCCTTCTATGCCCGCCTGTGCCCGGGGTCCCAGGGCGCCCTGTGCGCGCCTTGGGCGCCCTGGCGCCCAG ACGTITETGAAGGGCCGTGCGGCGAGAGGCGTCCGAGCACTGCCAATGTGACGCGGGCCCACGGCCGCATCG STGCCAGTGAACCGCATCCTGCCCCACCCCAAGTTTGACCCGCGGACCTTCCACAACGACCTGGCCTGGTGC AGAGAGGCCCGTGTTCCCCTGCTCAGCACCGACACCTGCCGAAGAGCCCTGGGGGCCCGGGCTGCGCCCAGC <u> ACCATÓCTCTGCGCCGGGTACCTGGCGGGGGGGGTTGACTCGTGCCAGGGTGACTCGGGAGGCCCCCTGACC</u> FGTTCTGAGCCTGGCCCCCGCCCTAGAGAGGTCCTGTTCGGAGTCACCTCCTGGGGGGGCGGCTGCGGGGGAG CCAGGGAAGCCCGGGGTCTACACCCGCGTGGCAGTGTTCAAGGACTGGCTCCAGGAGCAGATGAGCGCAGCC TGCGGCGCGCGTCCTGGTAGCGGCCTCCTGGGTGCTCACGGCAGCGCACTGCTTTGTAGGCTGCCGCTCGACC

GCGCAGGAGCTGCTCGGGCCTCGTCCGGGACTGCGGCCCTGGCCCCCGCCCTGGCTCTCCCCGGCTCTCCCAGCG CTCAGGGAGTCTCCTCTGCACCCCGGCGCGGGGCTGCGGCTTCACTCAGGATCGCGGGCTGCAGGCACTCGGT TCCCGAAGCGGAGGCCGGAGCCGCGCGCGGAGAAGCCAACGGCTGCCCTGGGCTGGAGCCCCTGCGACAGAAGT AGGGCAGGGCCCGGGCTGGAGAGGAGGGGCACCACCACTCAACCCTCAGGTACCCCCCCGCCAGGCAACC GGTGCAGGCCCTGCAGGCCTTCCGCGTGGCTGCCCTGGCAGAGGGGGAGCCCGAGGGACCCTGGATGTG TGGCTGCCCTGCAGGGGCCCATGCCTGGATCCTGCAGGTCCCCTCGGAGCACCTGGCCATGAACTTTCATGA SCGGCATGTGGCCTTCAGCGGCCTGGTGGGCCTGGAGCCGGCCACACTGGCTCGCAGCCTCCCCCGGCTGCT GGTCCTGGCAGATCTGGGCTCCAAGACACTGACCGGGCTTTTCAGAGCCTGGGTGCGGGCAGGCTTGGGGGG

SGPR455 SEQID 42

TGTGGAATGTTGACCATCACTTCAATATTCAGTTCTAGTAACATGACGGTGATATACTTTAAAAAGTGATGGTAAAA STGAGAAGGCCCAAACACATAATAGTGCATGAAGACTTTAACACACTAAGTTATGACTCTGACATTGCCCTAATAC AATATTCAAATGTCCTACAAGAAATGGAACTTCCCATCATGGATGACAGAGCGTGTAATACTGTGCTCAAGAGCAT ATTTACAAGTTTAGACATGGAAAAGCAAGTTGGATGTGATCATGACTATGTATCTTTACGATCAAGCAGTGGAGTG 4AATTTAGTCCAAACTGTATTTATGATGCTGTTGTGATTTACGGTGATTCTGAAGAAAAGCACAAGTTAGCTAAACT CCCCAAAACAATCCTGTATCTACCGTAAAAGCTATTCTGCATGATGTCTGTGGCATCCCTCCATTTAGTCCCAG TGAAGAATAATĆCACTCTCCTGGACTATTATTGCTGGGGACCATGACAGAAACCTGAAGGAATCAACAGAGCAG CTGACAGCGATGATAAAGTTGAACCAGGAATTCTTTGCTTATCCAGTGGATGGGGCAAGATTTCCAAAACATCAG SAACCTCCCTCCCTGGGAAGGACCATGCTGTGTGCTGGCTTCCCTGATTGGGGAATGGACGCCTGCCAGGGG 4GGTTGTGGGAGTCTGGCTATATTGGTAGAAGAAGGGACAAATCACTCTGCCAAGTATCCTGATTTGTATCCCAG ATGAGTCCTGATATTGCACTGCTGTATCTAAAACACAAAGTCAAGTTTGGAAATGCTGTTCAGCCAATCTGTTCT GACTCTGGAGGACCACTGGTTTGTAGAAGAGGTGGTGGAATCTGGATTCTTGCTGGGATAACTTCCTGGGTAGC TGGTTGTGCTGGAGGTTCAGTTCCCGTAAGAACAACCATGTGAAGGCATCACTTGGCATTTTCTCCAAAGTGTC GAGTTGATGGATTTTATCACTCAAAACCTGTTCACAGGTTTGGATCGGGGCCAACCCCTCTCAAAAGTGGGCTC
 AAGGTATATAACAAAGGCCCTGAGTTCTGTCCAAGAAGTGAATGGAAGCCAGAGAGATAAAATAATCCTGATAAA
VTCGTTTACAAGGCTTCAAGGCCAGATTTACCATTTTGCCCTCAGAGTCTTTAAACAAATTTGAACCAAAGTTACC 'GGCTTTCCAGAAGAATCGCAGGAGGGGAAGAAGCCTGCCCCCACTGTTGGCCATGGCAGGTGGGTCTGAGGT TCTAGGCGATTACCAATGTGGAGGTGCCATCATCAACCCAGTGTGGATTCTGACCGCAGCCCACTGTGTGCAA STITCTGATACAGAAGACAGTGGCAGTGGCTTTGAGCTTACCGTTACTGCTGTACAGAAGTCAGAAGCAGGGTC CTTTTTAGTAAGGTCTGTGGAAAAATATTGCCTTCACCATTGCTGGCAGAGACCAGTGAGGCCATGGTTCCATTT

FIG. 1LL

ATGCAGATCCCAAGAAATTCTCACAGAACTACTATGGGTTGCCAATGGAGATTAGTAGCCCCTTTAAATCACATCA 4GACTTTCCCAAAGTTCAAACAGAGAGCACTTGGTCCCTTGTGAGGATGTTCTTCTGACCAAGCCAGAAGGGATC ATTTGGACCAGGAAAAAAATTAATAGGTAGAATGTTGATGAGCACTGAGCTTTCTTGGTTCCTAAGCCAATTCAGC 36GAGCTGGCTGTGCCAGCCATGGAAGCCGGGTGTATTTGCCAGAGTGATGATCTTCTTGGACTGGATCCATAT SGTGGATTACATGGAAGAAGACTTTACTCAATGACTTTCATGAGTCCTGGACCGCTGGTGAGGGTGACATTCCAT STGCCCATCCAGGAGGGATCACAGAGAAGATGATCTGTGCTGGCTTTGCAGCATCTGGAGAGAAAGATTTCTGC AGTTGTTGCTCTGAAGCAGAGGCTAGAAAGCCTAGAGGCTTTTTCCCACACCACGGGTATCTACTGGATTATAGA GCCCTTGTACGAGGTGCATTTGGTATAAGCTATATTGTCTTGAAAGTCCTAGGTCCAAAGGACAGTAAAATAACC 3TGGCCTAGCAAGTCGCCTACAGCAGATTCAAGTGCATGTGTTAGAAAGAGAGGTCTGTGAACACACTTACTAT CAGGGAGACTCTGGTGGGCCACTAGTATGTAGACATGAAAATGGTCCCTTTGTCCTCTATGGCATTGTCAGCTG IACAGAACACCTGTTACCATGCACTGCCTCATGAGGTTGTTTTGAGAATTAAATAA

CTGCTCCCTATTTGGTGTACCTCAAGTCTCACTTCAACCCCTGTGTGGGCGTCCTCATCAAACCCAGCTGGGTGC GCTCATCAAGCTGGCTAAGCCTGCCATGCTCAATCCCAAAGTCCAGCCCCTTACCCTCGCCACCACCAATGTCA SGCCAGGCACTGTCTGTCTACTCTCAGGTTTGGACTGGAGCCAAGAAAAAAGGGGGTTTGGCAGCTGGAGCCA FGGCCCCAGCTCACTGCTATTTACCAAATCTGAAAGTGATGCTGGGAAATTTCAAGAGCAGAGTCAGAGACGGTA CTGAACAGACAATTAACCCCATTCAGATCGTCCGCTACTGGAACTACAGTCATAGCGCCCCACAGGATGACCTCA ACACCCTGACTTGCGGCAGAACCTGGAGGCCCCCGTGATGTCTGATCGAGAATGCCAAAAAAACAGGAACAAGGAA CCAGGCCATCTGACTCTGCACAGAGGCCCAGCCATTCCTGATTGGCAGAGACACAATTCACATGAACAAGGCCG AAAGCCACAGGAATTCCTTATGTGTGAAATTTGTGAAAGTATTCAGCCGAATTTTTGGGGAGGTGGCCGTTGCTA CTGTCATCTGCAAAGACAAGCTCCAGGGAATCGAGGTGGGGCACTTCATGGGAGGGGGGCGTCGGCATCTACAC CAATGTTTACAAATATGTATCCTGGATTGAGAACACTGCTAAGGACAAGTG/

>SGPR559 SEQID 44

SECCCTETEGATCATCACTECTECACACTGTGTTTATGACTTGTACCTCCCCAAGTCATGGACCATCCAGGTGG STCTAGTTTCCCTGTTGGACAATCCAGCCCCATCCCACTTGGTGGAGAAGATTGTCTACCACAGGAAGTACAAGC ATCATCGTCATTGGGATCATTGCATTGATATTAGCACTGGCCATTGGTCTGGGCATCCACTTCGACTGCTCAGGG <u> AAGTACAGATGTCGCTCATCCTTTAAGTGTATCGAGCTGATAGCTCGATGTGACGGAGTCTCGGATTGCAAAGAC</u> 36AAGACCATGTGCTCCGATGACTGGAAGGGTCACTACGCAAATGTTGCCTGTGCCCAACTGGGTTTCCCAAGC IATGTGAGTTCAGATAACCTCAGAGTGAGCTCGCTGGAGGGGGCAGTTCCGGGAGGAGTTTGTGTCCATCGATCA AGGATGGAGCAGGTGACGCCTCCCCTGTCCTGAACCACGCGGCCGTCCCTTTGATTTCCAACAAGATCTGCAAC CACAGGGACGTGTACGGTGGCATCATCTCCCCCTCCATGCTCTGCGCGGGCTACCTGACGGGTGGCGTGGACA SCTGCCAGGGGGACAGCGGGGGGCCCCTGGTGTGTCAAGAGAGGAGGCTGTGGAAGTTAGTGGGAGCGACCA GGGGAGGACGAGTACCGCTGTGTCCGGGTGGTGGTCAGAATGCCGTGCTCCAGGTGTTCACAGCTGCTTCGT STGTGCCTGCCCAACTCTGAAGAGAACTTCCCCGATGGAAAAGTGTGCTGGACGTCAGGATGGGGGGCCACAG CAAAGAGGCTGGGCAATGACATCGCCCTTATGAAGCTGGCCGGGCCACTCACGTTCAATGAAATGATCCAGCCT ATGGGGGAAAATGATCCGCCTGCTGTTGAAGCCCCCTTCTCATTCCGATCGCTTTTTGGCCTTGATGATTTGAAA TGCTCTCGCAGTGGCCCTGGCCAGCCATCCAGTTCCAGGGCTACCACCTGTGCGGGGGGTCTGTCATCA <u> ATAAGTCCTGTTGCACCAGATGCAGATGCTGTTGCTGCACAGATCCTGTCACTGCTGCCATTGAAGTTTTTCCA</u> CCACGAGCAGATGGAGAGAGGACCTAAAAACCTGA

FIG. 1NN

>SGPR567_1_SEQID_45

STAGCAGCAACTGGAATGACTCCTACTCAGAGAGACCTGCCAGCAGCTGGGTTTCGAGAGTGCTCACCGGACA CTCCAGCTGGGACACCTCCAGGCCGGGCATCTCCAGCCCAGGCATCTCCAGCCCAGGCATCTCCAGCTGGGAC CAGAGTGTACCTTGTTAGAGCAACACCAGTGGGGGCTGTACCCATCCGATCATCTCCTGCCAGGTCAGCACCAG CTGGCATCACTTTCCAGGTCCTCATCCGGCAGGTCATCATCCGCCAGGTCAGCCTCGGTGACAACCTCCCCAAC GCTGCGTGAGGTTTGACTGGGACAAGTCTCTGCTTAAAATCTACTCTGGGTCCTCCCATCAGTGGCTTCCCATCT 36CATCTCCAGCCCAGGCATCTCCAGCCCAGGCATCTCCAGCCCAGGCATCTCCAGCCCGGGCATCTCCGGCT CAACCAGGGCCACCAGGGAGAGCCCAGTCCAGTTCTGGCAGGGCCACACAGGGATCAGGTACAAGGAGCAGA SGGAGAGCTGTCCCAAGCACGCTGTTCGCTGTGACGGGGTGGTGGACTGCAAGCTGAAGAGTGACGAGCTGG ACCTCCGGGCCGGGCATCTCCAGCCCAGGCATCTCCAGCTGGTACACCTCCAGGCCGGGCATCTCCAGGCCG

TACACCAAAGTGACAGAAGTTCTTCCCTGGATTTACAGCAAGATGGAGAGCGAGGTGCGATTCAGAAAATCCTAA <u> CCACATCTGTGGAGGCACGCTCATTGACGCCCAGTGGGTGCTCACTGCCGCCCACTGCTTCTTCGTGACCCGG</u> GAGAAGGTCCTGGAGGGCTGGAAGGTGTACGCGGGCACCAGCAACCTGCACCAGTTGCCTGAGGCAGCTCC **ATTECCGAGATCATCATCAACAGCAATTACACCGATGAGGAGGACGACTATGACATCGCCCTCATGCGGCTGTC** GCGGATCGTGGGAGGGGCGCTGGCCTCGGATAGCAAGTGGCCTTGGCAAGTGAGTCTGCACTTCGGCACCAC GCAGGTCAATCTCATCGACTTCAAGAAATGCAATGACTACTTGGTCTATGACAGTTACCTTACCCCAAGGATGAT AGACCTGCTGGATCACAGGCTTTGGCAAGACCAGGGAGACAGATGACAAGACATCCCCCTTCCTCCGGGAGGT ACCGAGGTTGCCCACAGGGATTTTGCCAACAGCTTCTCAATCTTGAGATACAACTCCACCATCCAGGAAAGCCT

>SGPR479 1 SEQID 46

GCTGCGCACTGCTTTCACAGGGACAAGAATATCAAAATCTATGACATGTACGTAGGCCTCGTAAACCTCAGGGTG CGGAGGTGACGTGGCCCTGGTGCAGCTGAAGACCCGCATTGTGTTTTCTGAGTCCGTGCTCCCGGTTTGCCTTG GGCCTGTGGGTCGGCCCAGCATGGAGGGGAAAATCCTGGGCGGCGTCCCTGCGCCCCGAGAGAGGAAGTGGCCGTG GCCGGCAACCACACCAGTGGTATGAGGTGAACAGGGTGATCCTGCACCCCCACATATGAGATGTACCACCCCAT CAACTCCAGAAGTGAACCTTACCAGTGCCAATTGCTGGGCTACGGGATGGGGACTAGTCTCAAAACAAGGTGAG ACCTCAGACGAGCTGCAGGAGGTGCAGCTCCCGCTGATCCTGGAGCCCTGGTGCCACCTGCTTACGGACACA TGTCCTACATCATGCCCGACATGCTGTGTGCTGGGGACATCCTGAATGCTAAGACCGTGTGTGAGGGGGGGACTCC CCAACCCTCTGTACCCTGGAGTGTATGCCAGTGTTTCCTATTTCTCAAAATGGATATGTGATAACATAGAAATCAC GCCCACTCCTGCTCAGCCAGCCCCTGCTCTCTCTCCAGCTCTGGGGCCCACTCTCAGCGTCCTAATGGCCATGC GCAGGTCAGCGTGCACTACGCAGGCCTCCACGTCTGCGGCGGCTCCATCCTCAATGAGTACTGGGTGCTGTCA TGGCCCCTCCCCGGGTCGCAGCATTGGTCCACAGACAGCCAGAGAACCAGGGAATCTCCCTAACTGGCAGCGT GGGGGCCCACTTGTCTGTGAATTCAACCGCAGCTGGTTGCAGATTGGAATTGTGAGCTGGGGCCGAGGCTGCT TGGCTGGTCAGTGCTGTGA

>SGPR489_1_SEQID_47

CTGCAACTCTTTCGCTCCCCAAAGCTCCCAGTTGTGGGCAGAGTCTGGTTAAGGTACAGCCTTGGAATTATTTTA <u> ATGAGTCTCAAAATGCTTATAAGCAGGAACAAGCTGATTTTACTACTAGGAATAGTCTTTTTGAACGAGGTAAAT</u>

STCACTATTGAAACTGTCATCATACATCCACATTTCTCCACCAAGAAACCAATGGACTATGATATTGCCCTTTTGAA ACATTITCAGTCGCATTCTTGGAGGAAGCCAAGTGGAGAAGGGTTCCTATCCCTGGCAGGTATCTCTGAAACAAA GGCAGAAGCATATTTGTGGAGGAAGCATCGTCTCACCACAGTGGGTGATCACGGCGGCTCACTGCATTGCAAAC SATGGCTGGAGCCTTCCAATTTGGCCACTTTGTGGGGCCCATATGTCTTCCAGAGCTGCGGGGAGCAATTTGAGG STGTGGCACCTGGTGCAGTGAGCAGGATGTCATAGTCAGCGGGGCTGAGGGGGAAGCTGCACTTCCCAGAAAGC CAGGGGCTTTCAGGCTATAGTCTCCTTCATTCCTAAAGCAGTATACCCAGATTTAAACATCTCCATATCAGAGGAT GCCGGAATAAGAAAGGGGCCTGGGACTCTGGCTGGTCAATTTGGGAGGCTCAGGTGGGAGGATCGCTTGAGTC GACTGGATTTTCAAGCCTCCAAACATCACCTAATTAAGCTTTCATTTCAGAGTCTGGAAATAGAAGAAAGTGGAG CAGGAGTTCAAGACCAAGCCTAGGCAACAAGTGAGACTCTGTCTCACAAATAATTTCTTCAAAAAATTAGCCGG GGAAAATTTTGTGGAGAAAGCCTCCCTTCATCCATTCTTATTGGCTCTAATTCTCTAAGGCTGAAATTCGTCTCTG GATGTCCCCACCCCTGTGCTGAGCCCCTCCAGCATCATGCTCATCAGCTTCCATTCAGATGAAAACGGGACCTG CTTAACTGTCCTTTTTGAAGAAGGTCTCATACAGAGTCTAAACTATCCTGAAAACTACAGTGACAAGGCTAACTGT CTGGTTTTATTTGTACAACTGCAGGCTGGGGCCGCTTAACTGAAGGTGGCGTCCTCTCACAAGTCTTGCAGGAA STGAATCTGCCTATTTTGACCTGGGAAGAGTGTGTGGCAGCTCTGTTAACACTAAAGAGGGCCCATCAGTGGGAA GACCTTTCTTTGCACAGGTTTTCCTGATGGAGGGAGACGCATGTCAGGGAGATTCAGGAGGTTCACTCATGT CTCCACCTATATTATGAGAGCAAGCAACGGTGTGTCTGGACCCTGCTGGTACCAGAGGAAATGCATGTGTTGCT GAGTCAATGTTTCTGGAGACATGA

FIG. 1PP

>SGPR465 1 SEQID 48

ACTACACCATCCACGAGGACATGCTGTGCGCTGGGGACCTCATAACAGGAAAGGCCATTTGCCGAGTGAACTCC 4 G G G G T C C C T T C C C C A T T A A T G G C A C T G G T T C T G G G G C T G T G G A G C C T C G A C T G GATCATGGTGCACGCTGACTATAACGAGTTGCACCGCATGGGGAGTGACATCACCCTGCTGCAGCTGCACCATC GATTACCGGATCCTGCTTGGGTATGACCAGCAAAGCCATCCCACAGAGCACAGCAGCAGCAGATGACAGTGAATAA GGGTGGCCTCTGCTGCTCACTGCTTCCAAAGATGCATCTTCCCTCCACGGGCCCCGCTGTCCACTAACCCATCT CGGTGGCCATGGCAGGCCAGTCTCCTCTACCTAGGCGGGCACATCTGTGGAGCTGCCCTCATCGACAGCAAC1

CTCACCCGTCGGTCCCAGGGTCTTCACCAGGCTCCCCTACTTCACCAACTGGATCAGCCAGAAGAGAGGGGAGA CATCGTCCACAAGCCCGGGCTCTGCGCAGCCCTTCTGGCTGCTCACATGTTCCTCCTGCTGCTGATTCTCCTGG GCACCCCTCCAGATCCCGCCTTGGCTCCTCCTCAGGAACACCCCCCAGCCCTGGACAGCATGACCTCTCAGGG

>SGPR524 1 SEQID 49

TGGTCAAAGACATCACTGGCTTTGAAGGGAAAATTTCAAGCCCATATTACCCGAGCTACTATCCTCCAAAATGCA <u> ACTITIGGATIGITITIGICATGCCACGTGCCAAAGGCCACATCTTCTGTGAAGACTGTGTTGCCGCCATCTTGAA</u> AGTGTACCTGGAAATTTCAGACTTCTCTATCAACTCTTGGCATAGCACTGAAATTCTATAACTATTCAATAACCAAG STGTCCCTCAGGCCCAGCGTTGTGATGGAGTAAATGACTGCTTTGATGAAAGTGATGAACTGTTTTGCGTGAGGC 4CAAAGGCTGCTCTCAGTACTTCTATGCAGAGCATCTGTCTCTCCACTACCCGCTGGAGATTTCTGCAGCCTCAG SCTCATATACGGAGGCTCTCAGGAATCCGGGCATATTTTGAGGTCATTCCAGAACAAAAGTGTGAAAACACAGTG <u> CAGACAATITITCGAGTGCCCAGCCCTCTGGTTCACATTCAGCTCCAGTGCAGTTCAAGGCTTTCAGACAAGCCA</u> CTTTTGGCAGAATATGGCAGTTACAACATCAGTCAACCCTGCCCTGTTGGATCTTTTAGATGCTCCTCCGGTTTAT <u> ATGGACAAAGAAAACAGCGATGTTTCAGCCGCACCTGCTGACCTGAAAATATCCAATATCTCAGTCCAAGTGGTC</u> **AAAACAGAAAGCAAAGATGCTTTTTACTTTGCTGGGATGTTTCGCATCACCAACATTGAGTTTCTTCCCGAATACC** CTGCCTTCTCCAAATTTTATGAGCAGTCTGTTGTTGCAGATGTCAGCAGCAGCAACAAGAAGGCGGCCTCCTTGTCC <u> AGTGCCCAAAAGAAGCTGCCAGTGAGACGACCACCGTTGCCAGGGAGACGACTACCATTGCCAGGAAGACGAC</u> CACCACAAAGACCCATTGGCAAAGCCAAACCCAAGAAGCAATCCAAGAAAAAAAGTTCCCTTTTGGAATGTACAAA <u> ATAAAATCATTCTCTTCACAGTATTTTATTCATCCTAGCAGTCATAGCCTGGACACTTCTGTGGCTGTATATCAGI</u> SGACTCCATCCAGACAAGCATCATAAACCGGACCTCTGTGGGGGGGCTTGCAGGGACTGGCTGTGGACATGGAC STCAACCTGCCTGCAATACCAGCTCCTTCAGGCAGCATGGCCCTCTCATCTGTGATGGCTTCAGGGACTGTGAG SACAAAAGGAGTCCAGGGAATTTCTTTCAGTGTCACGGACTGTGCAGCAAGTGATAAACCTGGTTTATACAACAT CGAAGCCGACAACTGTGTCACTGACTCCCTGACCATTTACGACTCCCTTTTGCCCCATCCGGAGCAGCATCTTG GCTTTAGGAAACAAAATGCAAAATGTGATGGGACAGTGGATTGTCCAGATGGAAGTGATGAAGAAGGCTGCAC ACAGAATTTGTGAACCCACAAGAACATTAATGTCATTTGTTTCTACAAATAATCTCATGTTGGTGACATTTAAGTCT **AATGGCCGGGATGAGCAAAACTGCACTCAAAGTATTCCATGCAACAACAGAACTTTTAAGTGTGGGCAATGATATT**

CATCACTTCTCGGATGCTCTGTGCAGGCATAATGTCAGGCAAGAGAGATGCCTGCAAAGGAGATTCGGGTGGAC CTTTATCTTGTCGAAGAAAAGTGATGGAAAATGGATTTTGACTGGCATTGTTAGCTGGGGACATGGATGTGGAC GAATGCCAAGTTTGTCTCCCCGGTGAGAAGTTGTGGTCCACGAGTACTATAACAGTCAGACTTTTGATTATGA TATTGCTTTGCTACAGCTCAGTATTGCCTGGCCTGAGACCCTGAAACAGCTCATTCAGCCAATATGCATTCCTCC AAAGGCTCCCTCGTTCTGCAGCAAGCGGAGGTAGAGCTCATTGATCAAACGCTCTGTGTTTCCACCTACGGGA1 GACCAAACTTTCCTGGTGTTTACACAAGGGTGTCAAACTTTGTTCCCTGGATTCATAAATATGTCCCTTCTTTT

>SGPR422 SEQID 50

CGGACAAAGCAACATATCAACTTAAGGACTTACGAGAGGACGACGAAAATTTGGTGTATTCTTTGAAAATGTAC AAACCTGGAATGTTCTGTGCCGGATATATGGAAGGAATTTATGATGCCTGCAGGGGTGATTCTGGGGGACCTTTA GTCACAAGGGATCTGAAAGATACGTGGTATCTCATTGGAATTGTAAGCTGGGGAGATAACTGTGGTCAAAAGGAC ATGACATTGAACAAAATTAAAGACCTTTTTGCAGGGAAAGGACAGTGGGATTTGGCACCCGAAGCAGAATGCTG CTITCTTTIGIGICACAGICCAGAGGAAGATGGIGIGAAAGTAGATGICATTATGGIGITCCAGTICCCCTCTA
 AAGCAAGTTGTGGTAAACGAGTTGTTCCATTAAACGTCAACAGAATAGCATCTGGAGTCATTGCACCCAAGGCGG
<u> AAGCCATGGATGATTGCCGTTCTCATTGTGTTGTCCCTGACAGTGGTGGCAGTGACCATAGGTCTCCTGGTTCAC</u> FGCATCCTTCCAACCAAATTTGACTGTCCACATCACAGGATTTGGAGCACTTTACTATGGTGGGGAATCCCAAAAT TTGTCACTGCAGCACACTGCTTCCAGAAGTATAAAAATCCACATCGATGGACTGTTAGTTTTGGAACAAAAATCAA CTGAACAAAGGGCAGTAAGAGAAGAAAATCCAAAGCATCTTAAATCAGAAGATAAGGAATTTAAGAGCCTTGC 36AGAGGCTCCAGGCCTGGGAGCAGGTCCTGCTGGTCACCAATGAGCTCATCAACAGGGGAGTTAACTGTCC **SCCTCCCTTAATGAAAAGAAATGTCAGAAGATTTATTATCCATGAGAAGTACCGCTCTGCAGCAAGAGAGTACGA** CAATAAATGCCTCATCAGTTCAAGTTAATGTGGCCATGGTCAAGAATGGCAATGTGGGGCCAGGTTCCGGAGCA TCCTAGTATTTGACCAAAAAAAGGAGTACTATCATGGCTCCTTTAAAATTTTAGATCCACAAATCAATAACAATT AAGCCTGGAGTCTACACACAAGTGACTTATTACCGAAACTGGATTGCTTCAAAAACAGGCATCTAA

1RR

>SGPR538 SEQID 51

GCAGTCTGTGGCTCCTGGGCGCTGGCCGTGGCCAGCGTGGCCCTGGGCTTCCGGCACACGTGTGGGGG STECTGGAGCCTTGGGCATCTCAGACTCACTCACCACAAGGGAGTAAACCTCACTGACATCAAACTCAACAGTTC CCTGCTGCCTCTCAGCCCATTTCCGGGACCTTGCAGGATGAGGAGATAACTTTGAGCTGCTCAGAGGCCAGCGC CTCTGTGCTAGCGCCACGCTGGGTGGTGACTGCTGCACATTGTATGCACAGTTTCAGGCTGGCCCGCCTGTCCA 1GAGGAAGCTCTGCTCCCTGCACTCCCCAAAACAGTATCTTTCAGAATAAACAGCGAAGACTTCTTGCTGGAAGC <u> ACTTCTGGTCAAGTTGTTTCCCTCAGATGCTCTGAGTGTGGAGCGAGGCCCCTGGCTTCCCGGATAGTTGGTGG</u> GCTGGCGGGTTCATGCGGGGCTGGTCAGCCACAGTGCCGTCAGGCCCCCACCAAGGGGCCTCTGGTGGAGAGGA CCAGGAGTTTGCTCAGCTCTCTCTAGACTGGGAGGCTTCCTGGAGGAGGCGTGGCAGCCCAGGAACAACTGC TCAGAGCAGAGCCTGGAGACCAGCAGCATCCCATTTCTCAGGCGGTGTGCTGGCGTTCCATGCGACGTGGCTG GCTACCTGGACGGAAGGGCTGATGCATGCCAGGGAGATAGCGGGGGCCCCCTAGTGTGCCCAGATGGGGACA TATCCCACACCCCCTCTACAGTGCCCAGAATCATGACTACGACGTCGCCCTCCTGAGGCTCCAGACCGCTCTC <u> GGGTGTCTGGCTGGGGCCACCCACCCTAGCCATACTTACAGCTCGGATATGCTCCAGGACACGGTGGTGCC</u> GCAAGTGAGGGATCAGCCACGCTGGCTCCTGGTCTGCCATGAGGGCTGGAGCCCCGCCCTGGGGCTGCAGAT GCAGTGCTGGGAGCCCTGGGGCTGCTGGCCGGTGCAGGTGTTGGCTCATGGCTCCTAGTGCTGTATCTGTGT AACTTCTCAGACACTGTGGGCGCTGTGTGCCTGCCGGCCAAGGAACAGCATTTTCCGAAGGGCTCGCGGTGC1

>SGPR527 1 SEQID 52

TCTCAGTCCTACCCAGGAAGAACCTGAAGATCTGGACTGCGGGCGCCCTGAGCCCTCGGCCCGCATCGTGGGG <u> ATGGCCCĞĞCACCTGCTCCTCCCCCTTGTGATGCTTGTCATCAGTCCCATCCCAGGAGCCTTCCAGGACTCAGC</u> GTGGCCGCCATCGTGGTGCCGGCCAACTACAGCCAAGTGGAGCTGGGCGCCGACCTGGCCCTGCTGCGCCTG SECTCAAACECECAGCCEGECACCTGGCCTTGGCAAGTGAGCCTGCACCATGGAGGTGGCCACATCTGCGGG SECACCECCTECTEGECCACCEGCTEGEGAGACGTCCAGGAGGCAGATCCTCTGCCTCTCCCCTGGGTGCTA SECTCCCTCATCECCCCTCCTGGGTCCTCTCCGCTGCTCACTGTTTCATGACGAATGGGACGCTGGAGCCCG

SCTTTCTGGACCCGAACAGCTCCGACAGCCCACCCCGCGACCTCGACGCCTGGCGCGTGCTGCTGCTCGCC GGGTTCAGAGCCTGGCCTTCCCACCCAGCCCCAGAAGACCCAGTCAGATCCCCAGGAGCCCAGGGAG SAGAACTGCACCATTGCCCTGCCTGAGTGCGGGAAGGCCCCGCGGCCAGGGGCCTGGCCCTGGGGGCCTGGGCCCAG TGTGGACGGAGAAACCGCCCTGGAGTTTTCACTGCTGTGGCTACCTATGAGGCATGGATACGGGAGCAGGTGAT <u> 20GCTGCCCGGAGACCCGCCGCGCGCGCTCTGCCTGCCTACCAGGAAAAGGAGGAGGTGGGCAGCTGCTGG</u> <u> ACTCATGGCCCATGGATCAGCCATGTGACTCGGGGGGCCTACCTGGAGGACCAGCTAGCCTGGGATTGGGGCC</u> SCTGCCCCCCAGTGGCTCCCCACACTGGCCCACTGGAGGCAGCAATCTCTGCCCCCCAGAACTGGCCAAGGCC <u> 2TGATGGGGAGGAGTGAGACACAGACTTGTCCCCCACACAGAGCATGGTGCCTGTGGCCTGCGGCTGGTGC</u> GCCCTCCCCATCAGCCCTGCCCATCTGTCTCCACCCGGGGGTATCCCCCCGGGGGCCAGCTGCTGGGTGTTG GGCTGGAAAGAACCCCAGGACCGAGTCCCTGTGGCTGCTGTGTCTCCATCTTGACACAACGAATCTGTGACTG TCACTCTCCAGATATTGCCAGGGATGCTGTGTGCTGGCTACCCAGAGGGCCGCAGGGACACCTGCCAGGGTGA STGATGGTGCCAGGATCCAGACCCTGCCATGGGGCGCTGGTGTCTGAAAGCTGGGTCTTGGCACCTGCCAGCT SCCGCGCGCGCGGGGGGGCGCCCTGGTGCAGCACGAGAACGCTTCGTGGGACAACGCCTCGGACCTGG SECTECTECAGCTGCGCACGCCCGTGAACCTGAGCGCGCGTTCGCGGCCCGTGTGCCTACCCCACCCGGAAC SECTECTCCAGTGGGGGTCCTGTGGCCTGGCTGGCAGAGGTGCATGTGGCTGGTGATCGAGTCTGCACTGG CAGCATCCGGCTGCCCCAGCACCTGGGACTCAGGCCCCCCCTGGCCCTCCTGGAGCTGAGCTCCCGGGTGGA SCTCTATCAGGGCATCCTGCCCCCTGGAACCCTCTGTGTCCTGTATGCAGAGGGGGCAGGAGAACAGGTGTGAG ATGACCTCAGCACCGCCCTCCTGTGCCAGATGACGGAAGGGTCCTGGATCCTCGTGGCCATGGCTGTTCAAG ACTACTTCCTGCCCGGGAGCCGCTGCCGCCTGGCCCGCTGGGGCCGCGGGGAACCCGCGCGTTGGCCCAGGC 36AGCCGGGAGCTGTTTGCTGCCATTGGTCCTGAAGAGGCCTGGATCTCCCAGACAGTGGGAGAGGGCCAACT <u> regegatecececatgeagtetacttectgetectgetgaetetectgatecagagetga</u>

ATGCCATCCGTGCGCTTCGGGGGCCAACATCACTGCGGAGGCTTCCTGCTGCGAGCCCGCTGGGTGTCTCGG CCGCCCACTGCTTCAGCCACAGAGACCTCCGCACTGGCCTGGTGGTGGTGGGGCGCCCACGTCCTGAGTACTGC GCCATGGGGCTCGGGTTGAGGGGCTGGGGACGTCCTCTGCTGACTGTGGCCACCGCCCTGATGCTGCCGTG GGAGCCCACCCAGCAGGTGTTTGGCATCGATGCTCTCACCACACCCCCGACTACCACCCCATGACCCACGCC

SGPR542 SEQID 53

<u> AGGAGCTGCCGCCTGGACTGATGGAGGCCAAGGTCCGAGTGCTGGACCCGGACGTCTGCAACAGCTCCTGGAA</u> GGGCCACCTGACACTTACCATGCTCTGCACCCGCAGTGGGGACAGCCACAGACGGGGGCTTCTGCTCGGCCGAC CCCAAGACCCCCGACGTGTACACGCAGGTGTCCGCCTTTGTGGCCTGGATCTGGGACGTGGTTCGGCGGGGCGAGCA AACGACATCTGCCTGCTGCAGCTGAACGGCTCTGCTGTCCTGGGCCCTGCAGTGGGGCTGCTGAGGCTGCCAG TCCGGAGGGCCCCTGGTGTGCAGGAACCGGGCTCACGGCCTCGTTTCCTTCTCGGGCCTCTGGTGCGGCGAC GTCCCCAGCCCGGCCCCCTGCGTGGACCACCAGGCCCCCAGGAGAAGCCGCCTGA

>SGPR551_SEQID_54

36CCAGTGGACGATCCAGAACAGGAGGCTGTGTGGCTTGCGCATCCTGCAGCCCTACGCCGAGAGGATCCCCG CAAAGAGGACAGCACATGCATCTCACTGCCCAAGGTCTGTGATGGGCAGCCTGATTGTCTCAACGGCAGCGATG STECTECTGCCCTGCTCGTGCTGGCTTCGGCGGGGGTGCTACTCTGGTATTTCCTAGGGTACAAGGCGGAGG GGACCTCATGCTCAAACTCCGGCTGGAGTGGACGCTGGCAGAGTGCCGGGACCGACTGGCCATGTATGACGTG FGGACTACGGCTTGGCCCTCTGGTTTGATGCCTATGCACTGAGGAGGCAGAAGTATGATTTGCCGTGCACCCAG A A GAGCAGT G C C A G G G G G G C C A T G T G G G A C A T T C A C T T C C A G T G A G G A C C G G A G C T G C G A G A A G A G A C C G G A G C T G C G T G C T G C A A G A A G A G A C A T C A C T T C A C T T C A G T T IGATGGTCAGCCAGGTGTACTCAGGCAGTCTGCGTGTACTCAATCGCCACTTCTCCCAGGATCTTACCCGCCGG GTCCACAGTCAACAGCTCGGCTGCCGTCCCCTACAGGGCCGAGTACGAAGTGGACCCCGAGGGGCCTAGTGATC CCTCAGCACCCCGTACTTCCCCAGCTACTACTCGCCCCAAACCCACTGCTCCTGGCACCTCACGGTGCCTCTC GETGGCCACGGCCGGGATCACCATCAACTTCACCTCCCAGATCTCCCTCACCGGGCCCGGTGTGCGGGTGCCA GAATCTAGTGCCTTCCGCAGTGAAACCGCCAAAGCCCAGAAGATGCTCAAGGAGCTCATCACCAGCACCCGCCT SCGTGCAGCCGGTGGTCTTCCAGGCCTGTGAAGTGAACCTGACGCTGGACAACAGGCTCGACTCCCAGGGCGT STGGCGTCGGGGGCCATCATGGCGGTCGTCTGGAAGAAGGGCCTGCACAGCTACTACGACCCCTTCGTGCTCT CTGGAAGCCAGTGTGAAAGACATAGCTGCATTGAATTCCACGCTGGGTTGTTACCGCTACAGCTACGTGGGCCA 36GCCAGGTCCTCCGGCTGAAGGGGCCTGACCACCTGGCCTCCAGCTGCCTGTGGCACCTGCAGGGCCCCAA CTATGGCTTGTACAACCAGTCGGACCCCTGCCCTGGAGAGTTCCTCTGTTCTGTGAATGGACTCTGTGTCCTG CCTGTGATGGGGTCAAGGACTGCCCCAACGGCCTGGATGAGAGAAACTGCGTTTGCAGAGCCACATTCCAGTG AGAGGGGATGTTCAAGGCCTGTGAGGACTCCAAGAGAAAAGCCCGGGGGTACCTCCGCCTGGTGCCCCTGTTT 2CAAATCCCCGAGCACCGCCGGCTGATGCTGAGCCCCGAGGTGGTGCAGGCACTGCTGGTGGAGGAGGTGCT SCCGGGCCCCTGGAGAAGAGGCTCATCACCTCGGTGTACGGCTGCAGCCGCCAGGAGCCCGTGGTGGAGGTT SCCCAACCCGCAGTGTGATGGGCGGCCCGACTGCAGGGACGGCTCGGATGAGGAGCACTGTGACTGTGGCCT

FIG. 1UU

<u> CCAGGGCCCCTCCAGCCGCATTGTTGGTGGAGCTGTGTCCTCCGAGGGTGAGTGGCCATGGCAGGCCAGGCCTC</u> rccaggaggacagcatggcctccacggtgctgtggaccgtgttcctgggcaaggtgtggcagaactcgcgctg SACETGECECTECTGCAGCTCGACCACCCGGTGGTGCGCTCGGCCGCCGTGCGCCCCGTTTGCCTGCCCGCG ATCAGCAACGCTCTGCAGAAAGTGGATGTGCAGTTGATCCCACAGGACCTGTGCAGCGAGGCCTATCGCTACCA CCGCTGGTGTGCAAGGCACTCAGTGGCCGCTGGTTCCTGGCGGGGCTGGTCAGCTGGGGCCTGGGCTGTGGC CAGGTTCGGGGTCGACACATCTGTGGGGGGGCCCTCATCGCTGACCGCTGGGTGATAACAGCTGCCCACTGCT GCCTGGAGAGGTGTCCTTCAAGGTGAGCCGCCTGCTCCTGCACCGTACCACGAAGAGGACAGCCATGACTAC CGGCCTAACTACTTCGGCGTCTACACCCGCATCACAGGTGTGATCAGGTGGATCCAGCAAGTGGTGACCTGA

>SGPR451_SEQID_55

A GTTA C G G A C A T G G C T G G G G G G G G T T T C C T G G T C T A T T G G G C C A T C T A C C A A A G T G G C T G CAGCCTATTTGCCTACCTTTTGATGTTTTCCAAATCCTGGACGGAAACACAAAGTGTTTTATAAGTGGCTGGGGAA SAACAAAAGAAGAAGGTAACGCTACAAATATTTTACAAGATGCAGAAGTGCATTATATTTCTCGAGAGATGTGTAA 4GTGAGAGAGAGGTGGGTCCTCACAGCTGCCCACTGCACTAAAGACACTAGCGATCCTTTAATGTGGACAGCTG FGATTGGA&CTAATAATATACATGGACGCTATCCTCATACCAAGAAGATAAAAATTAAAGCAATCATTATTCATCCA TCTGAGAGGAGTTATGGGGGAATAATTCCTAACACTTCATTTTGTGCAGGTGATGAAGATGGAGCTTTTGATACT \GGATTGTGGAACAGCACCGCTTAAGGATGTGTGCAAGGGTCTCGGATTATAGGGGGCACCGAAGCACAAGCT **AACTTCATTTTGGAATCTTATGTAAATGATATTGCACTTTTTCACTTAAAAAAAGCAGTGAGGTATAATGACTATAT** GCAGGGGTGACAGTGGGGGACCATTAATGTGCTACTTACCAGAATATAAAAGATTTTTTGTAATGGGAATTACC GGAGCTCTCACTTATACTCAGACCACTACTCGCCCTCTGGAAGGCACAGGCTCGGCCCCTCGCCGGAACCGGC GACCTGCCGCCATCTTGCTCACCAGCCTCCAAAATGCGGCTGGGGCTCCTGAGCGTGGCGCGTGTTGTTGTGG **FATGITITIGE CATCITACTAGCAACACATAA**

>SGPR452_1_SEQID_56

TGGGCAGCAGCTTGAAGTGGGCGTGGGCCAAGCCCTCTGGGATGCCCGTCCCAGAGAATGACCTGGTGGGCAT AGCCCCCGGCAGCCCAGGACCCCTGACTGTAGGCTCCAGGCCTCCCTGGAAGCCCTGGCACGCTCGCCCCG CAGCCCTCAGACTGGCTGTGCTTCGCGGATCTTGGCTGGTTCGAGGCTGATGGAGCTGCCCACTCCATGGGCC

SGTGCTGGAGAACGCCGTCTGTGAGCAGCCCTACCGCAACGCCTCAGGGCACACTGGCGACCGGCAGCTCATC TCTGGAAGGACACCGACCCGTCCATCTACCGGATCCACGCTGGGGACGTGTATCTCTACGGGGGCCGGGGG SCAGGCTGCGGGGGTCCTGGCGCCTGGTGGGGGTGGTCAGCTGGGGCTACGGCTGTACCCTGCGGGACTTTC STGGATGACATGCTGTGTGCCGGCAGCGAGGGCCGAGACTCCTGCTACGGTGACTCCGGCGGCGCCCTCTGGTCT TGTGGGGGGCCACAATGCCCCCCCGGGGAAGTGGCCGTGGCAGGTCAGCCTGAGGGTCTACAGCTACCACTG SCAGCTGCCGGGGTCACCTCTCCCCAGAGTCGCTGCCGCCGCCTACCGCCTGCAGCAGGCGAGTGTGCA FGCTGAACGTCAGCCGGATCATCGTCCACCCCAACTATGTCACTGCGGGGCTGGGTGCGGATGTGGCCTGCT GGCCTCCTGGGCGCACATCTGTGGGGGCTCCCTCATCCACCCCCAGTGGGTGCTGACTGCTGCCGCCACTGCATT SCGGCGTCTACACCCACGTCCAGATCTACGTGCTCTGGATCCTGCAGCAAGTCGGGGAGTTGCCCTGA

>SGPR504_SEQID_57

<u> ATCGGGGGCCACGAGGTGACCCCCCCACTCCAGGCCCTACATGGCATCCGTGCGCTTCGGGGGGCCAACATCACT</u> SCGGAGGCTTCCTGCTGCGAGCCCGCTGGGTGGTCTCGGCCGCCCAGTGCTTCAGCCACAGG

SGPR469 SEQID 58

<u>GGAGATT</u>CTGGGGGCCCCTGGTCTGTGAATTAAATGGCACATGGGTCCAGGTGGGGATTGTGAGCTGGGGCA

SGPR400 SEQID 59

SCCCAGTTTCTGTTAGCCCTGTTGTCCTGCTCATCTGCCTTCCCTCATCTGAAGTCTACCTGAAGAAGAATACAAC <u> SAGCATCCGCCAGGGCTTGATTCACGTCTGCTCAGATACCCTCATCTCAGAGGAGTGGGTGCTGACAGTGGCGA</u> CACGGGCACTGCTGGCTATGCATTCACGCTGCTCCTTCTGCTGGGGATTTCGGGTGAGCCCCCCAGAATGGGTCT STGGGCGGCCCACAGTCTCATCTGGTATTGCCTCAGGCTTGGGGGCTAGTGTGGGGGCAGTGGCCCTGGCAGG SAAAGTGCCCCTCATTGATCTCCAGACATGCGGTGACCACTATCAAAATGAAATCTTGCTGCACGGAGTTGAGCT STCCTGCTGGGTGACTGGATGGGGCTATACTGGAATATTCCAATATATCAAGCGTTCTTATACACTGAAGGAGCT SAGAGTCAGGTTCTTCCCGATTTGACAGCAGGGGACGCCGCAGACCCCCCCAATTCCTCCCTTGGGTCCTGGAG <u> ATTICICCITICITATAGAGCATCACTCCTTGCTGTTGTAACACACAGATCCAATAATAGTCGTGGGCGAGCTTTT</u> CATCATCAGTGAAGCTATGATCTGCTCCAAGCTCCCAGTGGGCAGATGGATCAGTGTACTGTAAGAATCCACC SCTCAGGCACCTTTCACAGGCCTTGCCTTCCCCAGTGA ngaasti .cezell

>SGPr397_SEQID_60

GLIHMFSIGRSYEGRCLFILKLGRRSRLKRAVWIDCGIHAREWIGPAFCQWFVKEALLTYKSDPAMRKMLNHLYFYIMP <u>MKCLGKRRGQAAAFLPLCWLFLKILQPGHSHLYNNRYAGDKVIRFIPKTEEEAYALKKISYQLKVDLWQPSSISYVSEG</u> VFNVDGYHFSWTNDRFWRKTRSRNSRFRCRGVDANRNWKVKWCGKFGTNWDPDPKVSAGFTLQNMSPEDSHGR TVTDVHIPQNGSRALLAFLQEANIQYKVLIEDLQKTLEKGSSLHTQRNRRSLSGYNYEVYHSLEEIQNWMHHLNKTHS

>SGPr413 SEQID 61

WTTDRLWRKSRSPHNNGTCFGTDLNRNFNASWCSIGASRNCQDQTFCGTGPVSEPETKAVASFIESKKDDILCFLTM MKPLLETLYLLGMLVPGGLGYDRSLAQHRQEIVDKSVSPWSLETYSYNIYHPMGEIYEWMREISEKYKEVVTQHFLGV HSYGQLILTPYGYTKNKSSNHPEMIQVGQKAANALKAKYGTNYRVGSSADILYASSGSSRDWARDIGIPFSYTFELRD TYETHPMYYLKISQPSGNPKKIIWMDCGIHAREWIAPAFCQWFVKEILQNHKDNSSIRKLLRNLDFYVLPVLNIDGYIYT SGTYGFVLPEAQIQPTCEETMEAVLSVLDDVYAKHWHSDSAGRVTSATMLLGLLVSCMSLL

>SGPr404 SEQID 62

YPHESQLPEEWENNRESLIVFMEQVHRGIKGLVRDSHGKGIPNAIISVEGINHDIRTANDGDYWRLLNPGEYVVTAKAE RNEMTTTDDLDFKHHNYKEMRQLMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHPGEHEVGEPEFHYIAGAHGNE LLWEAEDRQNVPRKVPNHYIAIPEWFLSENATVAAETRAVIAWMEKIPFVLGGNLQGGELVVAYPYDLVRSPWKTQEH VLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLPSLNPDGYEKAYEGGSELGGWSLGRWTHDGIDINNNFPDLNT MVSNDSHTWVTVKNGSGDMIFEGNSEKEIPVLNELPVPMVARYIRINPQSWFDNGSICMRMEILGCPLPDPNNYYHR PTPDDHVFRWLAYSYASTHRLMTDARRRVCHTEDFQKEEGTVNGASWHTVAGSLNDFSYLHTNCFELSIYVGCDK **GFTASTKNCMVGYDMGATRCDFTLSKTNMARIREIMEKFGKQPVSLPARRLKLRGRKRRQRG**

>SGPr536 1 SEQID 63

SSWAFSTAAVASDRVSIHSLGHMTPVLSPQNLLSCDTHQQGGCRGGRLDGAWWFLRRRGVVSDHCYPFSGRERDE CNRTVSDCCPDFWDFCLGVPPFFPPIQGCMHGGRIYPVLGTYWDNCNRCTCQENRQWQCDQEPCLVDPDMIKAIN AGPAPPCMMHSRAMGRGKRQATAHCPNSYVNNNDIYQVTPVYRLGSNDKEIMKELMENGPVQALMEVHEDFFLYK MWRCPLGL LLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQDLCCRGRADDCALPYLGAICYCDLF QGNYGWQAGNHSAFWGMTLDEGIRYRLGTIRPSSSVMNMHEIYTVLNPGEVLPTAFEASEKWPNLIHEPLDQGNCA 3GIYSHTPVSLGRPERYRRHGTHSVKITGWGEETLPDGRTLKYWTAANSWGPAWGERGHFRIVRGVNECDIESFVL

KYFMSPTLTMRLAGLSQITNQLHTFNDVCNNESLVSDTETSIAKELADWLISNNVVEHIFGPNLHIEIIKQCQVILNFLAAE MLMAFQNISDEQSFKAQSDHRSRHEVSHYSMWLLVSWAHCCSLVKSSLADSDHLQDWLKKLTLLIPETAVRHESCSG EYDLIGVTVHTGTADGGHYYSFIRDIVNPHAYKNNKWYLFNDAEVKPFDSAQLASECFGGEMTTKTYDSVTDKFMDFS athiaggsqescitrtgdflgetignelfncrqfigpqhhhhhhhhhhhdghmyddmlsaddyscsssqvsaksek /IORLRPVHAHLYLQPGMEDGSDDMDTSVEDIGGRSCVTRFVRTLLLIMEHGVKPHSKHLTEYFAFLYEFAKMGEEES **HSSRAAAYDLLVEMVKGSVENYRLIHNWVMAQHMQSHAPYKWDYWPHEDVRAECRFVGLTNLGATCYLASTIQQLY** _CVAKIFQIQFPLYTAYKHNTHPTIEDISTQESNILGAFCDMNDVEVPLHLLRYVCLFCGKNGLSLMKDCFEYGTPETLP **GRLSTQHIDCIWAAAQLKHCSRYIHDLFPSLIKNLDPVPLRHLLNLVSALEPSVHTEQTLYLASMLIKALWNNALAAKAQ** -SKQSSFASLLNTNIPIGNKKEEEELRRTAPSPWSPAASPQSSDNSDTHQSGGSDIEMDEQLINRTKHVQQRLSDTEE SMQGSSDETANSGEDGSSGPGSSSGHSDGSSNEVNSSHASQSAGSPGSEVQSEDIADIEALKEEDEDDDHGHNPP DIVQDEDAVNLSEGLINEAEKLLCSLVCWFTDRQIRMRFIEGCLENLGNNRSVVISLRLLPKLFGTFQQFGSSYDTHWI1 DALARHLADCIRSREILDHQDGNVEDDGLTGLLRLATSVVKHKPPFKFSREGQEFLRDIFNLLFLLPSLKDRQQPKCKS EMSPELKNTVKSLFGGVITNNVVSLDCEHVSQTAEEFYTVRCQVADMKNIYESLDEVTIKDTLEGDNMYTCSQCGKKV RAEKRACFKKLPRIXSFNTMRYTFNMVTMMKEKVNTHFSFPLRLDMTPYTEDFLMGKSERKEGFKEVSDHSKDSESY EKTHSAYMLFYKRMEPEEENGREYKFDVSSELLEWIWHDNMQFLQDKNIFEHTYFGFMWQLCSCIPSTLPDPKAVS KSSCGTDLRNRKLESQAGICLGDSQGTSERNGTSSGTGKDLVFNTESLPSVDNRMRMLDACSHSEDPEHDISGEMN NQQAQLQEFGQSNRKGEFPGGLMGPVRMISSGHELTTDYDEKALHELGFKDMQMVFVSLGAPRRERKGEGVQLPA -MTAKLSTSFVLETFIHSKEKPTMLQWIELLTKQFNNSQAACEWFLDRMADDDWWPMQILIKCPNQIVRQMFQRLCIH **ZFLLSLQAISTMVHFYMGTKGPENPQVEVLSEEEGGEEEEEEDILSLAEEKYRPAALEKMIALVALLVEQSRSERHLTL** SQTDMAALTGGKGFPFLFQHIRDGINIRQTCNLIFSLCRYNNRLAEHIVSMLFTSIAKLTPEAANPFFKLLTMLMEFAGG FLIAHAFITVVSNIRIWLHIPAVMQHIIPFRTYVIRYLCKLSDQELRQSAARNIMADLMWSTVKEPLDTTLCFDKESLDLAF MWAEKELINMMKLFFDNLVYYIQTVREGRQKHALYSHSAEVQVRLQFLTCVFSTLGSPDHFRLSLEQVDILWHCLVED SECYDDALHWFLNQVRSKDQHAMGMETYKHLFLEKMPQLKPETISMTGLNLFQHLCNLARLATSAYDGCSNSELCG MDQFWGIALRAQSGDVSRAAIQYINSYYINGKTGLEKEQEFISKCMESLMIASSSLEQESHSSLMVIERGLLMLKTHLE LYKLSLSGLDGGDSINRSFLLLAASTLLKFLPDAQALKPIRIDDYEEEPILKPGCKEYFWLLCKLVDNIHIKDASQTTLLDL MIPEARQAVFTAKYSEDMKHKTTLLELQKMFTYLMESECKAYNPRPFCKTYTMDKQPLNTGEQKDMTEFFTDLITKIE NMADFDGEESGCEEELVQINSHAELTSHLQQHLPNLASIYHEHLSQGPVVHKHQFNSNAVTDINLDNVCKKGNTLLW MCENCADLVEVLNEISDVEGGDGLQLRKEHTLKIFTYINSWTQRQCLCCFKEYKHLEIFNQVVCALINLVIAQVQVLRD **AFRRFAYHLRQWQIEGTGISSHLKALSDKQSLPLRVVCQPAGLPDKMTIEMYPSDQVADLRAEVTHWYENLQKEQI** SCLPPPQKDNIPMLLLLQEPHLTTLFDLLEMLASFKPPSGKVAVDDSESLRCEELHLHAENLSRRVWELLMLLPTCPN >SGPr414 SEQID 64

LORKDVKOALIOWOERIEFAHKLLTLLNSYSPPELRNACIDVLKELVLLSPHDFLHTLVPFLOHNHCTYHHSNIPMSLGP YFPCRENIKLIGGKSNIRPPRPELNMCLLPTMVETSKGKDDVYDRMLLDYFFSYHQFIHLLCRVAINCEKFTETLVKLSV LVAYEGLPLHLALFPKLWTELCOTOSAMSKNCIKLLCEDPVFAEYIKCILMDERTFLNNNIVYTFMTHFLLKVQSQVFSE LQEQEAKERKTKDDEGATPIKRRVSSDEEHTVDSCISDMKTETREVLTPTSTSDNETRDSSIIDPGTEQDLPSPENSS PPGMPPFASYILQRIWEVIEYNPSQCLDWLAVQTPRNKLAHSWVLQNMENWVERFLLAHNYPRVRTSAAYLLVSLIPS TYFMDLWNLFQPKLSEPAIATNHNKQALLSFWYNVCADCPENIRLIVQNPVVTKNIAFNYILADHDDQDVVLFNRGMLP ANCANLISTLITNLISQYQNLQSDFSNRVEISKASASLNGDLRALALLLSVHTPKQLNPALIPTLQELLSKCRTCLQQRNS **AYYGILRLCCEQSPAFTRQLASHQNIQWAFKNLTPHASQYPGAVEELFNLMQLFIAQRPDMREEELEDIKQFKKTTISC** VKEYRMEVPSSFSEDMSNIRSQHAEEQSNNGRYDDCKEFKDLHCSKDSTLAEEESEFPSTSISAVLSDLADLRSCDG NSFRQMFRSTRSLHIPTRDLPLSPDTTVVLHQVYNVLLGLLSRAKLYVDAAVHGTTKLVPYFSFMTYCLISKTEKLMFS YLRCLDGRSCWTTLISAFRILLESDEDRLLVVFNRGLILMTESFNTLHMMYHEATACHVTGDLVELLSIFLSVLKSTRPY QALPSQDPEVALSLSCGHSRGLFSHMQQHDILDTLCRTIESTIHVVTRISGKGNQAAS

· CEEE

KFNRLPRVLILHLKRYSFNVALSLNNKIGQQVIIPRYLTLSSHCTENTKPPFTLGWSAHMAMSRPLKASQMVNSCITSPS FLSIDKVPSKDAEEMRLFLDAVHQNRLPAAMKPSQGSGSFGAILGSRTSQKETSRQLSYSDNQASAKRGSLETKDDIP FRKVLGNPGRGSIKTVAGSGIARTIPSLTSTSTPLRSGLLENRTEKRKRMISTGSELNEDYPKENDSSSNNKAMTDPSR DVFDMEYTEAEAEELKRNAETGNLPHSYRLISVVSHIGSTSSSGHYISDVYDIKKQAWFTYNDLEVSKIQEAAVQSDRD MSPLKIHGPIRIRSMQTGITKWKEGSFEIVEKENKVSLVVHYNTGGIPRIFQLSHNIKNVVLRPSGAKQSRLMLTLQDNS LVKKDICNSETKKDLLKKVKNAISATAERFSGYMQNDAHEFLSQCLDQLKEDMEKLNKTWKTEPVSGEENSPDISATR AYTCPVITNLEFEVQHSIICKACGEIIPKREQFNDLSIDLPRRKKPLPPRSIQDSLDLFFRAEELEYSCEKCGGKCALVRH KYLTSSREKQLSLKQSEENRTSGGLLPLQSSSFYGSRAGSKEHSSGGTNLDRTNVSSQTPSAKRSLGFLPQPVPLSV TPSKKFTFKSKSSLALCLDSDSEDELKRSVALSQRLCEMLGNEQQQEDLEKDSKLCPIEPDKSELENSGFDRMSEEEL KKLRCNQDYTGWNKPRVPLSSHQQQQLQGFSNLGNTCYMNAILQSLFSLQSFANDLLKQGIPWKKIPLNALIRRFAHL -AAVLEISKRDASPSLSHEDDDKPTSSPDTGFAEDDIQEMPENPDTMETEKPKTITELDPASFTEITKDCDENKENKTP EGSQGEVDWLQQYDMEREREEQELQQALAQSLQEQEAWEQKEDDDLKRATELSLQEFNNSFVDALGSDEDSGNE RSGYIFFYMHKEIFDELLETEKNSQSLSTEVGKTTRQAS

FNNDGVCCCLQKRGPVNITSVCVSPRTLQISVFVLSEKYEGIVKFESDELPFGVIGSNIGDAHFQEFRAGISWKPVVDP DDPIPQFPDCCSSSSSRIPSVSVLVAVPLVAGHKGQAFIERMLGCFKELKQELTQEGPGGGHPRSAWPPRRHAQWP MTLLAPWYTGPMIPMDVNEPSSVTTAPTLSSSLQHISSFLATGKKLSLHFGHPRECEVTRIDDKNRRGLEDSEPGAKL

PGRRAELKLEPEPEPVREAEQEPKQELEDENPARSGGGGNSDEVPPPTLPSDPPRPPDPSPRRSRAPRRPRPRPQ **ASSKESRMNGQLQLPTNSGNNENKYSLFAVVNHQGTLESGHYTSFIRHHKDQWFKCDDAVITKASIKDVLDSEGYLLF** FFLSDRHRCEMPSPELCLVCEMSSLFRELYSGNPSPHVPYKLLHLVWIHARHLAGYRQQDAHEFLIAALDVLHRHCKG LQASTSTEVSHQQCSVPGLGEKFPTWETTKPELELLGHNPRRRRITSSFTIGLRGLINLGNTCFMNCIVQALTHTPILRD TLTDCLRRFTRPEHLGSSAKIKCGSCQSYQESTKQLTMNKLPVVACFHFKRFEHSAKQRRKITTYISFPLELDMTPFM TRLRTPPQPRPRPPRPPRPRRGPGGCLDVDFAVGPPGCSHVNSFKVGENWRQELRVIYQCFVWCGTPETRKSKA KSCICHVCGTHLNRLHSCLSCVFFGCFTEKHIHEHAETKQHNLAVDLYYGGIYCFMCKDYVYDKDIEQIAKEEQGEALK DDVGKAANNPNHCNCIIDQIFTGGLQSDVTCQACHGVSTTIDPCWDISLDLPGSCTSFWPMSPGRESSVNGESHIPGI PEPCEQGEEPPPVEAEEVEEAETAEKAERKVEAEAKVEGKAEAAGKAEAAGKVDATEKVETAGKVDAAGKVETAEG YHKQVLEHESEKVKEMNTQAY

COSSSIT. CSSSII

>SGPr495 SEQID 67

-NISNNLCFLEGKHLRSYSPQNAFQTLSQSYITTSKECSIQSCLYQFTSMELLMGNNKLLCENCTKNKQKYQEETSFAE MRVKDPTKALPEKAKRSKRPTVPHDEDSSDDIAVGLTCQHVSHAISVNHVKRAIAENLWSVCSECLEERRFYDGQLVL DSEPSESESASKQTGLFRSSSGSGVQPDGPLYPLSAGKLLYTKETDSGDKEMAEAISELRLSSTVTGDQDFDRENQP KKVEGVYTNARKQLLISAVPAVLILHLKRFHQAGLSLRKVNRHVDFPLMLDLAPFCSATCKNASVGDKVLYGLYGIVEH <u>ASILKAFNNPTTKTADDETRKKVKISTVKDPFIDISLPIIEERVSKPLLWGRMNKYRSLRETDHDRYSGNVTIENIHQPRA</u> **QTSAFSRIMKLCEEKCETDEIQKGGKCRNLSVRGITNLGNTCFFNAVMQNLAQTYTLTDLMNEIKESSTKLKIFPSSDS AKKHSSSKDKSQLIHDRKCIRKLSSGETVTYQKNENLEMNGDSLMFASLMNSESRLNESPTDDSEKEASHSESNVDA QLDPLVVELSRPGPLTSALFLFLHSMKETEKGPLSPKVLFNQLCQKAPRFKDFQQQDSQELLHYLLDAVRTEETKRIQ** SGSMREGHYTAYVKVRTPSRKLSEHNTKKKNVPGLKAADSESAGQWVHVSDTYLQVVPESRALSAQAYLLFYERVL TSDIWLCLKCGFQGCGKNSESQHSLKHFKSSRTEPHCIIINLSTWIIWCYECDEKLSTHCNKKVLAQIVDFLQKHASKT

>SGPr407 SEQID 68

MEYPVPYFRSPNRTLIPERIWSNPLLVLVIAYKTVSWPRQQLLAKQANKWMPFVIPSKTLPWDPLELKICYQQNRPYPS PDPSNFPTFLRCLNAFSAAVFYLPQPSWHKPEGLKPAGYPRVPDIPYGSGYTLKSTTEAAGLHQSLPMVQLPLHPTKG KAGKLFQPDAHGFLVKKVHAPTRGIVFIMEPRQLGGKGSLSKLQPACALGGMNSGMEPQKSAPFAAGKGLAPPLPVC VSLRDCLSLFTKEEELELENASGTLPVTKSEVLSTSCVPFGTTQAASTVATTQPCASARLVGTFTMTLVSPLNTLRDTE GIELTVMKALVLDILFKASTDIILFNHDSSSGNKWRKLPEPGGLEKKHEELRLRPLKEEYHWLVLVPLKLTGSPHRWRP SALLKESELNDADWANLMWKRYLEEQEDSKMVDLFVGQMKSYLKCQACGYHSMTFKVFFFCDLSLTIPKKGFAGGK RKRALASCSWCL QRVTMRRVMGV QDKAGNRN QMLLL G QRPVIGDTVSNS QTTR DKACRRPPSHSVFT QSSFWACL DPDLFFYGHQSYWMKAHLNDLILREGPVTQMAQSFYWGFPAGGNLSALEMLPDGPAPRTFLQKKSCLFPLFSYILLH

NLRFKLRVYKFEEELWSRAGLGKKSDNHSSRQMPWGAAGVACQHPCKLPRIVAELTPPKLSFGFLNTVQSSVLPTSL SQFFLNDSQPEEAIPPQSLLPGSPRTNSFPKDKFVPKDKLKVILSLLTMYELDRLF

>SGPr453 SEQID 69

NIFHGQLLSQVTCLACDNKSNTIEPFWDLSLEFPERYQCSGKDJASQPCLVTEMLAKFTETEALEGKIYVCDQCNSKRR **RRILMGKIFRTWFEQSPIGRKKQEEPFQEKIVVKREVKKRRQELEYQVKAELESMPPRKSLRLQGLAQSTIIEIVSVQVP** VMHHGKGFGSGHYTAYCYNSEGGFWVHCNDSKLSMCTMDEVCKAQAYILFYTQRVTENGHSKLLPPELLLGSQHPN RFSSKPVVLTEAQKQLMICHLPQVLRLHLKRFRWSGRNNREKIGVHVGFEEILNMEPYCCRETLKSLRPECFIYDLSAV VFCYLCDDYVLNDNATGDLKLLRRTLSAIKSQNYHCTTRSGRFLRSMGTGDDSYFLHDGAQSLLQSEDQLYTALWHR MTASEKTRSCKHPPVTDTVVYQMNECQEKDTGFVCSRQSSLSSGLSGGASKGRKMELIQPKEPTSQYISLCHELHTL FQVMWSGKWALVSPFAMLHSVWRLIPAFRGYAQQDAQEFLCELLDKIQRELETTGTSLPALIPTSQRKLIKQVLNVVN MLAMDTCKHVGQLQLAQDHSSLNPQKWHCVDCNTTESIWACLSCSHVACGRYIEEHALKHFQESSHPVALEVNEMY AQTPASPAKDKVLSTSENEISQKVSDSSVKRRPIVTPGVTGLRNLGNTCYMNSVLQVLSHLLIFRQCFLKLDLNQWLA

>SGPr445_SEQID_70

MRVKDPTKALPEKAKRSKRPTVPHDEDSSDDIAVGLTCQHVSHAISVNHVKRAIAENLWSVCSECLEERRFYDGQLVI OTSAFSRIMKLCEEKCETDEIQKGGKCRNLSVRGITNLGNTCFFNAVMQNLAQTYTLTDLMNEIKESSTKLKIFPSSDS *SDIWLCLKCGFQGCGKNSESQHSLKHFKSSRTEPHCIIINLSTWIIWCYECDEKLSTHCNKKVLAQIVDFLQKHASKT **QLDPLVVELSRPGPLTSALFLFLHSMKETEKGPLSPKVLFNQLCQKRVHLHL**

SGPr401 1 SEQID 71

MTVRNIASICNMGTNASALEKDIGPEQFPINEHYFGLVNFGNTCYCNSVLQALYFCRPFRENVLAYKAQQKKKENLLTC EAQKRMRVKKLPMVLALHLKRFKYMEQLRRYTKLSYRVVFPLELRLFNTSSDAVNLDRMYDLVAVVVHCGSGPNRGH LADLFHSIATQKKKVGVIPPKKFISRLRKENDLFDNYMQQDAHEFLNYLLNTIADILQEEKKQEKQNGKLKNGNMNEPA ENNKPELTWVHEIFQGTLTNETRCLNCETVSSKDEDFLDLSVDVEQNTSITHCLRDFSNTETLCSEQKYYCETCCSKQ YITIVKSHGFWLLFDDDIVEKIDAQAIEEFYGLTSDISKNSESGYILFYQSRE

>SGPr408 SEQID 72

SDYVSQSYSYSSILNKSETGYVGLVNQAMTCYLNSLLQTLFMTPEFRNALYKWEFEESEEDPVTSIPYQLQRLFVLLQT MVPGEENQLVPKEAPLDHTSDKSLLDANFEPGKKNFLHLTDKDGEQPQILLEDSSAGEDSVHDRFIGPLPREGSVGST SKKRAIETTDVTRSFGWDSSEAWQQHDVQELCRVMFDALEQKWKQTEQADLINELYQGKLKDYVRCLECGYEGWRI

GLEKNSLIYELFSVMAHSGSAAGGHYYACIKSFSDEQWYSFDDQHVSRITQEDIKKTHGGSSGSRGYYSSAFASSTNA VNNDRSTSSVDSDILSSSHSSDTLCNADNAQIPLANGLDSHSITSSRRTKANEGKKETWDTAEEDSGTDSEYDESGKS DTYLDIPLVIRPYGSSQAFASVEEALHAFIQPEILDGPNQYFCERCKKKCDARKGLRFLHFPYLLTLQLKRFDFDYTTMH KTWKNPGTVFLDYHIYEEDINISSNWEVFLEVLDGVEKMKSMSQLAVLSRRWKPSEMKLDPFQEVVLESSSVDELREK EAVEMAYKMMDLEEVIPLDCCRLVKYDEFHDYLERSYEGEEDTPMGLLLGGVKSTYMFDLLLETRKPDQVFQSYKPG FVESSETLDYQMAFADSHLWKLLDRHANTIRLFVLLPEQSPVSYSKRTAYQKAGGDSGNVDDDCERVKGPVGSLKSV EAILEESTEKLKSLSLQQQQDGDNGDSSKSTETSDFENIESPLNERDSSASVDNRELEQHIQTSDPENFQSEERSDSD YMLIYRLKDPARNAKFLEVGEYPEHIKNLVQKERELEEQEKRQREIERNTCKIKLFCLHPTKQVMMENKLEVHKDKTLK LSEISGIPLDDIEFAKGRGTFPCDISVLDIHQDLDWNPKVSTLNVWPLYICDDGAVIFYRDKTEELMELTDEQRNELMKK EVMVKVHVVDLKAESVAAPITVRAYLNQTVTEFKQLISKAIHLPAETMRIVLERCYNDLRLLSVSSKTLKAEGFFRSNKV SSFSDDNKITIRLGRALKKGEYRVKVYQLLVNEQEPCKFLLDAVFAKGMTVRQSKEELIPQLREQCGLELSIDRFRLRK RIKLNDRMTFPEELDMSTFIDVEDEKSPQTESCTDSGAENEGSCHSDQMSNDFSNDDGVDEGICLETNSGTEKISKS RGEMQYMYFKAEPYAADEGSGEGHKWLMVHVDKRITLAAFKQHLEPFVGVLSSHFKVFRVYASNQEFESVRLNETL ESSRLQKTGHRVTYSPRKEKALKIYLDGAPNKDLTQD

>SGPr480_SEQID_73

NLIVGLVLLTRGKDEEKAKYIFSLFSSESGNYVIREEMERMLHVVDGKVPDTLRKCFSEGEKVNYEKFRNWLFLNKDAF PSPNAPLKRVLAYTGCFSRMQTIKEIHEYLSQRLRIKEEDMRLWLYNSENYLTLLDDEDHKLEYLKIQDEQHLVIEVRNK KRTPQLIHGRDYEMVPEPVWRALYHWYGANLALPRPVIKNSKTDIPELELFPRYLLFLRQQPATRTQQSNIWVNMGNV JMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFMNSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHM MGAKESRIGFLSYEEALRRVTDVELKRLKDAFKRTCGLSYYMGQHCFIREVLGDGVPPKVAEVIYCSFGGTSKGLHFN GHNWFIISMQWWQQWKEYVKYDANPVVIEPSSVLNGGKYSFGTAAHPMEQVEDRIGSSLSYVNTTEEKFSDNISTAS EASETAGSGFLYSATPGADVCFARQHNTSDNNNQCLLGANGNILLHLNPQKPGAIDNQPLVTQEPVKATSLTLEGGRI DWEVAAEAWDNHLRRNRSIVVDLFHGQLRSQVKCKTCGHISVRFDPFNFLSLPLPMDSYMHLEITVIKLDGTTPVRYG KNRPSLFGMPLIVPCTVHTRKKDLYDAVWIQVSRLASPLPPQEASNHAQDCDDSMGYQYPFTLRVVQKDGNSCAWC SPSTNEMFTLTTNGDLPRPIFIPNGMPNTVVPCGTEKNFTNGMVNGHMPSLPDSPFTGYIIAVHRKMMRTELYFLSSQ RLNMDEKYTGLKKOLSDLCGLNSEQILLAEVHGSNIKNFPQDNQKVRLSVSGFLCAFEIPVPVSPISASSPTQTDFSS PWYRFCRGCKIDCGEDRAFIGNAYIAVDWDPTALHLRYQTSQERVVDEHESVEQSRRAQAEPINLDSCLRAFTSEEEI AKCYGDLVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQQDSQELLAFLLDGLHEDLNRVHEKPYVELKDSDGRP FFSRWLLSGGVYVTLTDDSDTPTFYQTLAGVTHLEESDIIDLEKRYWLLKAQSRTGRFDLETFGPLVSPPIRPSLSEGL FNAFDENRDNHIDFKEISCGLSACCRGPLAERQKFCFKVFDVDRDGVLSRVELRDMVVALLEVWKDNRTDDIPELHM DLSDIVEGILNAHDTTKMGHLTLEDYQIWSVKNVLANEFLNLLFQVCHIVLGLRPATPEEEGQIIRGWLERESRYGLQA

KGRLRLPQIGSKNKLSSSKENLDASKENGAGQICELADALSRGHVLGGSQPELVTPQDHEVALANGFLYEHEACGNG YSNGQLGNHSEEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKNPNCKWYCYNDSSCKELHPDEIDTDSAY QGDELSEPRILAREVKKVDAQSSAGEEDVLLSKSPSSLSANIISSPKGSPSSSRKSGTSCPSSKNSSPNSSPRTLGRS GENEMYYCSKCKTHCLATKKLDLWRLPPILIIHLKRFQFVNGRWIKSQKIVKFPRESFDPSAFLVPRDPALCQHKPLTP LFYEQQGIDYAQFLPKTDGKKMADTSSMDEDFESDYKKYCVLQ

>SGPr431 SEQID 74

SETSLOEVASKAAVLTETPRTSDGEKTLIEKMFGGKLRTHIRCLNCRSTSQKVEAFTDLSLAFCPSSSLENMSVQDPAS MDKILEGLVSSSHPLPLKRVIVRKVVESAEHWLDEAQCEAMFDLTTRLILEGQDPFQRQVGHQVLEAYARYHRPEFES PKGKLSITFCQQLVRTIGHFQCVSTQERELREYVSQVTKVSNLLQNIWKAEPATLLPSLQEVFASISSTDASFEPSVALA NGCNSLMKKLQHLFAFLAHTQREAYAPRIFFEASRPPWFTPRSQQDCSEYLRFLLDRLHEEEKILKVQASHKPSEILEC TPSVTDLLNYFLAPEILTGDNQYYCENCASLQNAEKTMQITEEPEYLILTLLRFSYDQKYHVRRKILDNVSLPLVLELPVK YHQSEALALASSQSHLLGRDSPSAVFEQDLENKEMSKEWFLFNDSRVTFTSFQSVQKITSRFPKDTAYVLLYKKQHST FFNKTFVLGLLHQGYHSLDRKDVAILDYIHNGLKLIMSCPSVLDLFSLLQVEVLRMVCERPEPQLCARLSDLLTDFVQCI RITSFSSLSESWSVDVDFTDLSENLAKKLKPSGTDEASCTKLVPYLLSSVVVHSGISSESGHYYSYARNITSTDSSYQM NGLSGNNPTSGLWINGDPPLQKELMDAITKDNKLYLQEQELNARARALQAASASCSFRPNGFDDNDPPGSCGPTGG RLWFPLVRPGALAVLSHMLLSFQHSPEAFHLIVPHVVNLVHSFKNDGLPSSTAFLVQLTELIHCMMYHYSGFPDLYEPI SLVQHIPLQMITVLIRSLTTDPNVKDASMTQALCRMIDWLSWPLAQHVDTWVIALLKGLAAVQKFTILIDVTLLKIELVFN LEAIKDFPKPSEEKIKLILNQSAWTSQSNSLASCLSRLSGKSETGKTGLINLGNTCYMNSVIQALFMATDFRRQVLSLNI SPSIQDGGLMQASVPGPSEEPVVYNPTTAAFICDSLVNEKTIGSPPNEFYCSENTSVPNESNKILVNKDVPQKPGGET **GGGGENTVGRLVF**

FIG. 2G

>SGPr429_SEQID_75

PSKSQTRKPKCGKGTHCSRNAYMLVYRLQTQEKPNTTVQVPAFLQELVDRDNSKFEEWCIEMAEMRKQSVDKGKAK HEEVKELYQRLPAGAEPYEFVSLEWLQKWLDESTPTKPIDNHACLCSHDKLHPDKISIMKRISEYAADIFYSRYGGGPR SKFYELELNIQGHKQLTDCISEFLKEEKLEGDNRYFCENCQSKQNATRKIRLLSLPCTLNLQLMRFVFDRQTGHKKKLN YIGFSEILDMEPYVEHKGGSYVYELSAVLIHRGVSAYSGHYIAHVKDPQSGEWYKFNDEDIEKMEGKKLQLGIEEDLE MAPRLQLEKAAWRWAETVRPEEVSQEHIETAYRIWLEPCIRGVCRRNCKGNPNCLVGIGEHIWLGEIDENSFHNIDDP NCERRKKNSFVGLTNLGATCYVNTFLQVWFLNLELRQALYLCPSTCSDYMLGDGIQEEKDYEPQTICEHLQYLFALLQ .TVKALCKECVVERCRILRLKNQLNEDYKTVNNLLKAAVKGDGFWVGKSSLRSWRQLALEQLDEQDGDAEQSNGKM NSNRRYIDPSGFVKALGLDTGQQQDAQEFSKLFMSLLEDTLSKQKNPDVRNIVQQQFCGEYAYVTVCNQCGRESKLL NGSTLNKDESKEERKEEEELNFNEDILCPHGELCISENERRLVSKEAWSKLQQYFPKAPEFPSYKECCSQCKILEREG

GLMFTFASMTKEDSKLIALIWPSEWQMIQKLFVVDHVIKITRIEVGDVNPSETQYISEPKLCPECREGLLCQQQRDLREY EENEALHKMIANEQKTSLPNLFQDKNRPCLSNWPEDTDVLYIVSQFFVEEWRKFVRKPTRCSPVSSVGNSALLCPHG RHRKVRGEKALLVSANQTLKELKIQIMHAFSVAPFDQNLSIDGKILSDDÇATLGTLGVIPESVILLKADEPIADYAAMDDV TOATIYVHKVVDNKKVMKDSAPELNVSSSETEEDKEEAKPDGEKDPDFNQSNGGTKRQKISHQNYIAYQKQVIRRSM MQVCMPEEGFKGTGLLGH

COSSSSIN . OSSSSI

>SGPr503 SEQID 76

MNSLLQGLSACPAFIRWLEEFTSQYSRDQKEPPSHQYLSLTLLHLLKALSCQEVTDDEVLDASCLLDVLRMYRWQISS PVLNQPGAPKTQIFMNGACSPSLLPTLSAPMPFPLPVVPDYSSSTYLFRLMAVVVHHGDMHSGHFVTYRRSPPSARN CKHCEHQSPVRFDTFDSLSLSIPAATWGHPLTLDHCLHHFISSESVRDVVCDNCTKIEAKGTLNGEKVEHQRTTFVKQ -KLGKLPQCLCIHLQRLSWSSHGTPLKRHEHVQFNEFLMMDIYKYHLLGHKPSQHNPKLNKNPGPTLELQDGPGAPT MLSSRAEAAMTAADRAIQRFLRTGAAVRYKVMKNWGVIGGIAAALAAGIYVIWGPITERKKRRKGLVPGLVNLGNTCF FEEQDAHELFHVITSSLEDERDRQPRVTHLFDVHSLEQQSEITPKQITCRTRGSPHPTSNHWKSQHPFHGRLTSNMV PLSTSNQWLWVSDDTVRKASLQEVLSSSAYLLFYERVLSRMQHQSQECKSEE

>SGPr427 SEQID 77

REDEVNTRGAYILFYQKRNSIPPWSASSSMRGSTSSSLSDHWLLRLGSHAGSTRGSLLSWSSAPCPSLPQVPDSPIF SQSIVSLLTGTAGEDEKSASPRSNVALPANSEDGGRAIERGPAGVPCPSAQPNHCLAPGNSDGPNTARKLKENAGQD RALWTREYTPQLSAEFKNAVSKYGSQFQGNSQHDALEFLLWLLDRVHEDLEGSSRGPVSEKLPPEATKTSENCLSPS SCTLDECFQFYTKEEQLAQDDAWKCPHCQVLQQGMVKLSLWTLPDILIIHLKRFCQVGERRNKLSTLVKFPLSGLNMA PHVAQRSTSPEAGLGPWPSWKQPDCLPTSYPLDFLYDLYAVCNHHGNLQGGHYTAYCRNSLDGQWYSYDDSTVEP MDLGPGDAAGGGPLAPRPRRRRSLRRLFSRFLLALGSRSRPGDSPPRPQPGHCDGDGEGGFACAPGPVPAAPGSP GEERPPGPQPQLQLPAGDGARPPGAQGLKNHGNTCFMNAVVQCLSNTDLLAEFLALGRYRAAPGRAEVTEQLAALV alrkmyaeeggvpadevilvelypsgfqrsffdeedlntiaegdnvyafqvppspsqgtlsahplglsasprlaareg QRFSLSLHSESKVLILFCNLVGSGQQASRFGPPFLIREDRAVSWAQLQQSILSKVRHLMKSEAPVQNLGSLFSIRVVGL AQLPLGQSFVQSHFQAQYRSSLTCPHCLKQSNTFDPFLCVSLPIPLRQTRFLSVTLVFPSKSQRFLRVGLAVPILSTVA SVACSYLSPKDSRPLCHWAVDRVLHLRRPGGPPHVKLAVEWDSSVKERLFGSLQEERAQDADSVWQQQQAHQQH KLPRKFDLPLTVMPSVEHEKPARPEGQKAMNWKESFQMGSKSSPPSPYMGFSGNSKDSRRGTSELDRPLQGTLTL RSVFRKKENRRNERAEVSPQVPPVSLVSGGLSPAMDGQAPGSPPALRIPEGLARGLGSRLERDVWSAPSSLRLPR INSLCNQEKGGLEPRRLVRGVKGRSISMKAPTTSRAKQGPFKTMPLRWSFGSKEKPPGASVELVEYLESRRRPRST *ASRAPRGSALGMSQRTVPGEQASYGTFQRVKYHTLSLGRKKTLPESSF*

>SGPr092_SEQID_78

WAHEDGWPFDGPGGILGHAFLPNSGNPGVVHFDKNEHWSASDTGYNLFLVATHEIGHSLGLQHSGNQSSIMYPTYW HQPHCGVPDGSDTSISPGRCKWNKHTLTYRIINYPHDMKPSAVKDSIYNAVSIWSNVTPLIFQQVQNGDADIKVSFWQ MQLVILRVTIFLPWCFAVPVPPAADHKGWDFVEGYFHQFFLTKKESPLLTQETQTQLLQQFHRNGTDLLDMQMHALI YHDPRTFQLSADDIQRIQHLYGEKCSSDIP

>SGPr359 SEQID 7

RHVQQIDAAVYLREPQKTLFFVGDEYYSYDERKRKMEKDYPKNTEEEFSGVNGQIDAAVELNGYIYFFSGPKTYKYDT FGLQVTGKLDQTTMNVIKKPRCGVPDVANYRLFPGEPKWKKNTLTYRISKYTPSMSSVEVDKAVEMALQAWSSAVPL GLAHSTDPSALMYPTYKYKNPYGFHLPKDDVKGIQALYGPRKVFLGKPTLPHAPHHKPSIPDLCDSSSSFDAVTMLGK SFVRINSGEADIMISFENGDHGDSYPFDGPRGTLAHAFAPGEGLGGDTHFDNPEKWTMGTNGFNLFTVAAHEFGHAL ELLLFKDRIFWRRQVHLRTGIRPSTITSSFPQLMSNVDAAYEVAERGTAYFFKGPHYWITRGFQMQGPPRTIYDFGFP MKVLPASGLAVFLIMALKFSTAAPSLVAASPRTWRNNYRLAQAYLDKYYTNKEGHQIGEMVARGSNSMIRKIKELQAF **EKEDVVSVVKSSSWIGC**

>SGPr104 1 SEQID 80

MNVALOELGAGSNMVEYKRATLRDEDAPETPVEGGASPDAMEVGFQKGTRQLLGSRTQLELVLAGASLLLAALLLGC -KHLLENTTFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLIEKIGGWNITGPWDQDNFMEVLKAVAGTYRATPFF WQNESLAAFRNHTACMEEQYNQYQVNGERLNGRQTLGENIADNGGLKAAYNAYKAWLRKHGEEQQLPAVGLTNHQ EEALGQLVWMDEKTRQAAKEKADAIYDMIGFPDFILEPKELDDVYDGYEISEDSFFQNMLNLYNFSAKVMADQLRKPP LVALGVQYHRDPSHSTCLTEACIRVAGKILESLDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQAI TVYISADSKSSNSNVIQVDQSGLFLPSRDYYLNRTANEKVLTAYLDYMEELGMLLGGRPTSTREQMQQVLELEIQLANI NLVQKTTSSLDRRFESAQEKLLETLYGTKKSCVPRWQTCISNTDDALGFALGSLFVKATFDRQSKEIAEGMISEIRTAF SRDQWSMTPQTVNAYYLPTKNEIVFPAGILQAPFYARNHPKALNFGGIGVVMGHELTHAFDDQGREYDKEGNLRPW TVPQDQRRDEEKIYHKMSISELQALAPSMDWLEFLSFLLSPLELSDSEPVVVYGMDYLQQVSELINRTEPSILNNYLIW LFFVGFAQVWCSVRTPESSHEGLVTDPHSPARFRVLGTLSNSRDFLRHFGCPVGSPMNPGQLCEVW

>SGPr303_SEQID_81

MPEKRPFERLPADVSPINCSLCLKPDLLDFTFEGKLEAAAQVRQATNQIVMNCADIDIITASYAPEGDEEIHATGFNYQN EDEKVTLSFPSTLQTGTGTLKIDFVGELNDKMKGFYRSKYTTPSGEVRYAAVTQFEATDARRAFPCWDERAIKATFDIS ALEVAAKTLPFYNDYFNVPYPLPKIDLIAIADFAAGAMENWDLVTYRETALLIDPKNSCSSSRQWVALVVGHELAHQWF LVVPKDRVALSNMNVIDRKPYPDDENLVEVKFARTPVTSTYLVAFVVGEYDFVETRSKDGVCVCVYTPVGKAEQGKF

GNLVTMEWWTHLWLNEGFASWIEYLCVDHCFPEYDIWTQFVSADYTRAQELDALDNSHPIEVSVGHPSEVDEIFDAIS YSKGASVIRMLHDYIGDKVKKKTLSI

COMMONTS CENTSOL

>SGPr402_1_SEQID_82

/VQQSLTPHWGHHLHLKKNPKVQWFQQQTLQRRVKRSVVVPTDPWFSKQWYMNSEAQPDLSILQAWSQGLSGQGI VVSVLDDGIEKDHPDLWANYDPLASYDFNDYDPDPQPRYTPSKENRHGTRCAGEVAAMANNGFCGVGVAFNARIGG LGQLCLAYCPPRFFNHTRLVTAGPGHTAAPALRVCSSCHASCYTCRGGSPRDCTSCPPSSTLDQQQGSCMGPTTPD WRPAPIALWLRLVLALALVRPRAVGWAPVRAPIYVSSWAVQVSQGNREVERLARKFGFVNLGPIFPDGQYFHLRHRG VRMLDGTITDVIEAQSLSLQPQHIHIYSASWGPEDDGRTVDGPGILTREAFRRGVTKGRGGLGTLFIWASGNGGLHYD **ALALEANPFLTWRDMQHLVVRASKPAHLQAEDWRTNGVGRQVSHHYGYGLLDAGLLVDTARTWLPTQPQRKCAVR** MSTHFWDENPQGVWTLGLENKGYYFNTGTLYRYTLLLYGTAEDMTARPTGPQVTSSACVQRDTEGLCQACDGPAYI VQSRPTPILPLIYIRENVSACAGLHNSIRSLEHVQAQLTLSYSRRGDLEISLTSPMGTRSTLVAIRPLDVSTEGYNNWVF NCNCDGYTNSIHTLSVGSTTQQGRVPWYSEACASTLTTTYSSGVATDPQIVTTDLHHGCTDQHTGTSASAPLAAGMI SRPRLRAAACPHHRCPASAMVLSLLAVTLGGPVLCGMSMDLPLYAWLSRARATPTKPQVWLPAGT

>SGPr434 SEQID 83

CATNYGENLCYGDSGGPLACEVEGRWILAGVLSWEKACVKAQNPGVYTRITKYTKWIKKQMSNGAFSGPCASACLLF GPGROGGCAGRRSTALPLRAPLRARRPGPRSERMGAATCRGSRIPSGPPVQGERSAPRFGVTSLSLWPADFKDNW RIAGSRQEVALAGEPADQQQTHLRRLPYRQTLGYKEDTTNPVCGEPWWSEDLEMTRHWPWEVSLRMENEHVCGG QPICLPEPNFNLKVGTQCWVTGWSQVKQRESGSTANSMLTPELQEAEVFIMDNKRCDRHYKKSFFPPVVPLVLGDMI 4LIDPSWVVTAAHCSQGTKEYSVVLGTSKLQPMNFSRALWVPVRDIIMHPKYWGRAFIMGDVALVHLQTPVTFSEYV

>SGPr446 1 SEQID 84

VVSVQRAFVHPKFSTVTTIRNDLALLQLQHPVNFTSNIQPICIPQENFQVEGRTRCWVTGWGKTPERGEKLASEILQDV LTPVCGRTPLRIVGGVDAEEGRWPWQVSVRTKGRHICGGTLVTATWVLTAGHCISSRFHYSVKMGDRSVYNENTSV DQYIMCYEECNKIIQKALSSTKDVIIKGMVCGYKEQGKDSCQGDSGGRLACEYNDTWVQVGIVSWGIGCGR

>SGPr447 SEQID 85

QKHYYPSEWTVQLGELTSRPTPWNLRAYSSRYKVQDIIVNPDALGVLRNDIALLRLASSVTYNAYIQPICIESSTFNFVH MGARGAL_LALLLARAGLGKPEACGHREIHALVAGGVESARGRWPWQASLRLRRRHRCGGSLLSRRWVLSAAHCF

COMMOLT CONTOL

RPDCWVTGWGLISPSGTPLPPPYNLREAQVTILNNTRCNYLFEQPSSRSMIWDSMFCAGAEDGSVDTCKGDSGGPL VCDKDGLWYQVGIVSWGMDCGQPNRPGVYTNISVYFHWIRRVMSHSTPRPNPSQLLLLLALLWAP

-PGMVCTSAVGELPSCEGLSGAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVSSLDWQVYFAEEP YDMALLLLAQPVTLGASLRPLCLPYPDHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPI GASCWATGWDQDTSDAPGTLRNLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPVL NQSNSIFGCIFYTLQLLLGLQAAQRACGQRGPGPPKPQEGNTVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAH **CFEKAAATELNSWSVVLGSLQREGLSPGAEEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAHRFPF** CLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSPETPEMSDEDSCVACGSLRTAGPQ AGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHCFIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGG >SGPr432_1_SEQID_86 MGSTWGSPGWVRLALCLTGLVLSLYALHVKAARARDRDYRALCDVGTAISCSRVFSSRWGRGFGLVEHVLGQDSII EPEAEPGSCLANISQPTSC

>SGPr529_SEQID_87

DQSWVLTAAHCGNKPLWARVGDDHLLLLQGEQLRRTTRSVVHPKYHQGSGPILPRRTDEHDLMLLKLARPVVPGPR <u> MRAPHLHLSAASGARALAKLLPLLMAQLWAAEAALLPQNDTRLDPEAYGAPCARGSQPWQVSLFNGLSFHCAGVLV</u> VRALQLPYRCAQPGDQCQVAGWGTTAARRVKYNKGLTCSSITILSPKECEVFYPGVVTNNMICAGLDRGQDPCQSD SGGPLVCDETLQGILSWGVYPCGSAQHPAVYTQICKYMSWINKVIRSN

QYDDLNMHLEKLRVVQISRKECAKRVNQLSRNMICAWNEPGTNGQGPGEVGGPLVCQKKNKSTWYQLGIISWGVGC NVQCGHRPAFPNSSWLPFHERLQVQNGECPWQVSIQMSRKHLCGGSILHWWWVLTAAHCFRRTLLDMAVVNVTVV MGTRTFSNIHSERKQVQKVIIHKYYKPPQLDSDLSLLLLATPVQFSNFKMPVCLQEEERTWDWCWMAQWVTTNGYD **SQKNMPGVYTELSNYLLWIERKTVLAGKPYKYEPDSVYALLLSPWAILLLYFVMLLLS**

>SGPr425_SEQID_89

EDYLSYETVFENGTRTLTRVKVQDLVLEPTQNITTKGVSVRRKRQVYGTDSRFSILDKRFLTNFPFSTAVKLSTGCSGIL MENMLLWLIFFTPGWTLIDGSEMEWDFMWHLRKVPRIVSERTFHLTSPAFEADAKMMVNTVCGIECQKELPTPSLSEL SPQHVLTAAHCVHDGKDYVKGSKKLRVGLLKMRNKSGGKKRRGSKRSRREASGGDQREGTREHLPERAKGGRRR KKSGRGQRIAEGRPSFQWTRVKNTHIPKGWARGGMGDATLDYDYALLELKRAHKKKYMELGISPTIKKMPGGMIHFS

OSMESIE OFESIA

GFDNDRADQLVYRFCSVSDESNDLLYQYCDAESGSTGSGVYLRLKDPDKKNWKRKIIAVYSGHQWVDVHGVQKDYN VAVRITPLKYAQICLWIHGNDANCAYG

>SGPr548 SEQID 90

TTSRVIPHPRYEARSHRNDIMLLRLVQPARLNPQVRPAVLPTRCPHPGEACVVSGWGLVSHNEPGTAGSPRSQVSLP DTLHCANISIISDTSCDKSYPGRLTNTMVCAGAEGRGAESCEGDSGGPLVCGGILQGIVSWGDVPCDNTTKPGVYTKV MGDPEGSAEWGWGKGIPVVRRNLLTVDGISLCLEGSWWRQKGPASPGFSHSLPRLQPNPGPSSTMWLLLTLSFLLA STAAQDGDKLLEGDECAPHSQPWQVALYERGRFNCGASLISPHWVLSAAHCQSRFMRVRLGEHNLRKRDGPEQLR CHYLEWIRETMKRN

>SGPr396 SEQID 91

MGPAGCAFTLLLLLGISVCGQPVYSSRVVGGQDAAAGRWPWQVSLHFDHNFICGGSLVSERLILTAAHCIQPTWTTFS **VSWGLECGKSLPGVYTNVIYYQKWINATISRANNLDFSDFLFPIVLLSLALLRPSCAFGPNTIHRVGTVAEAVACIQGWE** YTVWLGSITVGDSRKRVKYYVSKIVIHPKYQDTTADVALLKLSSQVTFTSAILPICLPSVTKQLAIPPFCWVTGWGKVKE SSDRDYHSALQEAEVPIIDRQACEQLYNPIGIFLPALEPVIKEDKICAGDTQNMKDSCKGDSGGPLSCHIDGVWIQTGV ENAWRFSPRGR

>SGPr426 SEQID 92

KPSFRLTRCGIRMTSSNMPLPASSSTQRIVQGRETAMEGEWPWQASLQLIGSGHQCGASLISNTWLLTAAHCFWKNK VDDGPIQNTLRQARVETISTDVCNRKDVYDGLITPGMLCAGFMEGKIDACKGDSGGPLVYDNHDIWYIVGIVSWGQSC refiershqiermmsrifrhssvggrfikshviklspdeqgvdilivlifrypstdsaeqikkkiekalyqslktkqlsltin MMYAPVEFSEAEFSRAEYQRKQQFWDSVRLALFTLAIVAIIGIAIGIVTHFVVEDDKSFYYLASFKVTNIKYKENYGIRSS DPTQWIATFGATITPPAVKRNVRKIILHENYHRETNENDIALVQLSTGVEFSNIVQRVCLPDSSIKLPPKTSVFVTGFGSI ALPKKPGVYTRVTKYRDWIASKTGM

>SGPr552 SEQID 93

RIAEGLDAEEGEWPWQASLPQNNVYRRGATWLSNSWLITAAHCFIRVHDPKEWNVILSNPQTQSNIKNVIIQENYHYP AHDNDIAVVHLSSPVLYTSNIQKACLPDVNYIFLYNSEAVVTAWGSFKPLRTTSNVLHKGLVKIIDNRTCNNGEADGRVI TSGMLCAGFLEPRVDACQGDSGGPLVGTDSKGILAKGSLLVLKAGVNERALPNKPSVYTQVTYY

>SGPr405 SEQID 94

MVSKGGVAAEPEPHYCEDSERGPNTLTGPGSLPRGGGIEVGMEFPGCSGEGCVKPHEEAAREGAGRGKRAVPGPK **WPLSLWEATVKVRSNVLCNQTCRRRFPSNHTERFERLIKDDMLCAGDGNHGSWPGDNGGPLLCRRNCTWVQVEVV** <u> SKMAEFNWSMAFKGPAAGHEERLNSVSSRAKKGIGWDVAAASLRGVDHFSDLPPPLQVREELEACAFRVQVGQLRL</u> <u> MRTRACERMYHKGPTAHGQVTIIKAAMPCAGRKGQGSCQAALRTEDLTPTTPNTEVSPRADPRLSQPEDIWPEWAW</u> RRQQGSAEGPAAGWTLEQETRGDVLEDKNERADEEILRLAPGKGRLPIDSKHLKPVISSFPVRSQELGEGAGAGTLR ³ETSWQGANHADAQRPAGRVPTMQRPRDMGQGQEWVCRPFTHVTCYPTAIPRPFTHVTCYLMAVPSTLTHVTCYP PVVVGTTMLLLLLFLAVSSLGSCSTGSPAPVPENDLVGIVGGHNTPGEVVVAVGADRRSLHFPEGHRPVHLPDSHQG SNADCERQTYDAFPGAGDRKFIQDDMICAGRTGRRTWKGDSGGPLVCKKKGTWLQAGVVSWGFYSDRPSIGVYTR YEDDQRTKVVEIVRHPQYNESLSAQGGADIALLKLEAPVPLSELIHPVSLPSASLDVPSGKTCWVTGWGVIGRGELLP **FAVPRPFTHVTCYLMAVPSTLTHITCYMMAVPRPFTHITCYPMAVPSTLTHVTCHPTAIPRPFTHITCYTMAIPRPSTTP** CVSVRGPGAAECQPDRRPPNYSVFFLGADIALLKLATSSLEFTDSDNCWNTGWGMVGLLDMLPPPYRPQQVKVLTL SWGKLCGLRGYPGMYTRVTSYVSWIRQPCPSAQTPAVVRRFVLPPNPDVEALTPSVMGSGAPLPPAPDLQEAEVPI PATRRPSPAPSPTSPATRWPSPGPSPMSPATR

>SGPr485_1_SEQID_95

.LLLASPIKLDDLKVPICLPTQPGPATWRECWVAGWGQTNAADKNSVKTDLMKAPMVIMDWEECSKMFPKLTKNMLC AGYKNESYDACKGDSGGPLVCTPEPGEKWYQVGIISWGKSCGEKNTPGIYTSLVNYNLWIEKVTQLEGRPFNAEKRR *PWQVSIQVRSEPFCGGSILNKWWILTAAHCLYSEELFPEELSVVLGTNDLTSPSMEIKEVASIILHKDFKRANMDNDIA MLLFSVLLLLSLVTRTQLGPRTPLPEAGVAILGRARGAHRPQPPHPPSPVSECGDRSIFEGRTRYSRITGGMEAEVGE SVKQKPMGSPVSGVPEPGSPRSWLLLCPLSHVLFRAILY

>SGPr534 SEQID 96

SVRTSDVVVAGEFDQGSDEENIQVLKIAKVFKNPKFSILTVNNDITLLKLATPARFSQTVSAVCLPSADDDFPAGTLCAT FGWGKTKYNANKTPDKLQQAALPLLSNAECKKSWGRRITDVMICAGASGVSSCMGDSGGPLVCQKDGAWTLVGIVS MASLWLLSCFSLVGAAFGCGVPAIHPVLSGLSRIVNGEDAVPGSWPWQVSLQDKTGFHFCGGSLISEDWVVTAAHC *NGSRTCSTTTPAVYARVTKLIPWVQKILAAN*

>SGPr390 SEQID 97

NPPEGRNSEHIRTSARTNSGHTIFKKCNTQPFLSTQGFHVDHTAELRGIRWTSSLRRETSDYHRTLTPTLEALLHFLLR MEPTVADVHLVPRTTKEVPALDAACCRAASIGVVATSLVVLTLGVLLGGMNNSRHAALRAATLPGKVYSVTPEASKT

DPTKWVAYVGATYLSGSEASTVRAQVVQIVKHPLYNADTADFDVAVLELTSPLPFGRHIQPVCLPAATHIFPPSKKCLIS GWGNTQEGNATKPELLQKASVGIIDQKTCSVLYNFSLTDRMICAGFLEGKVDSCQGDSGGPLACEEAPGVFYLAGIVS GWGYLKEDFRKHLPRPAMVKPEVLQKATVELLDQALCASLYGHSLTDRMVCAGYLDGKVDSCQGDSGGPLVCEEPS WGIGCAQVKKPGVYTRITRLKGWILEIMSSQPLPMSPPSTTRMLATTSPRTTAGLTVPGATPSRPTPGAASRVTGQPA NSTLSAVSTTARGOTPFPDAPEATTHTOLPDCGLAPAALTRIVGGSAAGRGEWPWQVSLWLRRREHRCGAVLVAER WLLSAAHCFDVYGDPKQWAAFLGTPFLSGAEGQLERVARIYKHPFYNLYTLDYDVALLELAGPVRRSRLVRPICLPEP PLQTLSLGLEEELLQRGIRARLREHGISLAAYGTIVSAELTGRHKGPLAERDFKSGRCPGNSFSCGNSQCVTKVNPEC <u>DDQEDCSDGSDEAHCECGLQPAWRMAGRIVGGMEASPGEFPWQASLRENKEHFCGAAIINARWLVSAAHCFNEFQ</u> GRFFLAGIVSWGIGCAEARRPGVYARVTRLRDWILEATTKASMPLAPTMAPAPAPSTAWPTSPESPVVSTPTKSMQ ALSTVPLDWVTVPKLQECGARPAMEKPTRVVGGFGAASGEVPWQVSLKEGSRHFCGATVVGDRWLLSAAHCFNHT KVEQVRAHLGTASLLGLGGSPVKIGLRRVVLHPLYNPGILDFDLAVLELASPLAFNKYIQPVCLPLAIQKFPVGRKCMIS APRPPDGTRCVITGWGSVREGGSMARQLQKAAVRLLSEQTCRRFYPVQISSRMLCAGFPQGGVDSCSGDAGGPLA CREPSGRWVLTGVTSWGYGCGRPHFPGVYTRVAAVRGWIGQHIQE

>SGPr521 SEQID 98

<u> MARSLLLPLQILLLSLALETAGEEAQGDKIIDGAPCARGSHPWQVALLSGNQLHCGGVLVNERWVLTAAHCKMNEYTV</u> HLGSDTLGDRRAQRIKASKSFRHPGYSTQTHVNDLMLVKLNSQARLSSMVKKVRLPSRCEPPGTTCTVSGWGTTTS PDVTFPSDLMCVDVKLISPQDCTKVYKDLLENSMLCAGIPDSKKNACNGDSGGPLVCRGTLQGLVSWGTFPCGQPN **DPGVYTQVCKFTKWINDTMKKHR**

>SGPr530 1 SEQID 99

HQTQHTQKMSVHRIITHPDFEKLHPFGSDIAMLQLHLPMNFTSYIVPVCLPSRDMQLPSNVSCWITGWGMLTEDHKRV QLSPPFYLQEGKVGLIENTLCNTLYGQRTAKARPKLCTRRCCVGGYFSTGKSICKGDSGGPLVCYLPSAWVLVGLAS VSTVCGKPKVVGKIYGGRDAAAGQWPWQASLLYWGSHLCGAVLIDSCWLVSTTHCFLNKSQAPKNYQVLLGNIQLY **WGLDCRHPAYPSIFTRVTYFINWIDEIMRLTPLSDPALAPH**

PKFDPRTFHNDLALVQLWTPVSPGGSARPVCLPQEPQEPPAGTACAIAGWGALFEDGPEAEAVREARVPLLSTDTCR RALGPGLRPSTMLCAGYLAGGVDSCQGDSGGPLTCSEPGPRPREVLFGVTSWGDGCGEPGKPGVYTRVAVFKDWL >SGPr520_SEQID_100 MLLAVLLLLPLPSSWFAHGHPLYTRLPPSALQVFTLLLGAETVLGRNLDYVCEGPCGERRPSTANVTRAHGRIVGGSA QEQMSAASSSREPSCRELLAWDPPQELQADAARLCAFYARLCPGSQGACARLAHQQCLQRRRRCELRSLAHTLLGL APPGAWPWLVRLQLGGQPLCGGVLVAASWVLTAAHCFVGCRSTRSAPNELLWTVTLAEGSRGEQAEEVPVNRILPH

LRNAQELLGPRPGLRRLAPALALPAPALRESPLHPARELRLHSGSRAAGTRFPKRRPEPRGEANGCPGLEPLRQKLA ALQGAHAWILQVPSEHLAMNFHEVLADLGSKTLTGLFRAWVRAGLGGRHVAFSGLVGLEPATLARSLPRLLVQALQA FRVAALAEGEPEGPWMDVGQGPGLERKGHHPLNPQVPPARQP

MSPDIALL_YLKHKVKFGNAVQPICLPDSDDKVEPGILCLSSGWGKISKTSEYSNVLQEMELPIMDDRACNTVLKSMNLP ?LGRTMLCAGFPDWGMDACQGDSGGPLVCRRGGGIWILAGITSWVAGCAGGSVPVRNNHVKASLGIFSKVSELMDF EICAVTGWGSISAELSLNVSSLDGGLASRLQQIQVHVLEREVCEHTYYSAHPGGITEKMICAGFAASGEKDFCQGDSG FMSPGPLVRVTFHALVRGAFGISYIVLKVLGPKDSKITRLSQSSNREHLVPCEDVLLTKPEGIMQIPRNSHRTTMGCQW TQNLFTGLDRGQPLSKVGSRYITKALSSVQEVNGSQRDKIILIKFTSLDMEKQVGCDHDYVSLRSSSGVLFSKVCGKIL ³SPLLAETSEAMVPFVSDTEDSGSGFELTVTAVQKSEAGSGCGSLAILVEEGTNHSAKYPDLYPSNTRCHWFICAPEK HIIKLTFEDFAVKFSPNCIYDAVVIYGDSEEKHKLAKLCGMLTITSIFSSSNMTVIYFKSDGKNRLQGFKARFTILPSESLN (FEPKLPPQNNPVSTVKAILHDVCGIPPFSPQWLSRRIAGGEEACPHCWPWQVGLRFLGDYQCGGAIINPVWILTAAH RLVAPLNHIIQLNIINFPMKPTTFVCHGHLRVYEGFGPGKKLIGRMLMSTELSWFLSQFSTKKTTASCGETAVSMKMMY SVQLKNNPLSWTIIAGDHDRNLKESTEQVRRAKHIIVHEDFNTLSYDSDIALIQLSSPLEYNSVVRPVCLPHSAEPLFSS <PRGFFPTPRYLLDYRGRLECSWVLRVSASSMAKFTIEYLSLLGSPVCQDSVLIIYEERHSKRKTAGGLHGRRLYSMT</pre> 3PLVCRHENGPFVLYGIVSWGAGCVQPWKPGVFARVMIFLDWIQSKINGKLFSNVIKTITSFFRVGLGTVSCCSEAEL **TSIFLALQNTCYHALPHEVVLRIK**

-HRGPAIPDWQRHNSHEQGRHPDLRQNLEAPVMSDRECQKTEQGKSHRNSLCVKFVKVFSRIFGEVAVATVICKDKL QTINPIQIVRYWNYSHSAPQDDLMLIKLAKPAMLNPKVQPLTLATTNVRPGTVCLLSGLDWSQENSGLWQLEPPGHLT >SGPr507_2_SEQID_102 MKYVFYLGVLAGTFFFADSSVQKEDPAPYLVYLKSHFNPCVGVLIKPSWVLAPAHCYLPNLKVMLGNFKSRVRDGTE QGIEVGHFMGGDVGIYTNVYKYVSWIENTAKDK

>SGPr559 SEQID_103

KCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVFTAASWKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVS SLEGGFREEFVSIDHLLPDDKVTALHHSVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQ FQGYHLCGGSVITPLWIITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMKLAGPLT *NEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGAGDASPVLNHAAVPLISNKICNHRDVYGGIISPSMLCAGYLTG MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALILALAIGLGIHFDCSGKYRCRSSF 3VDSCQGDSGGPLVCQERRLWKLVGATSFGIGCAEVNKPGVYTRVTSFLDWIHËQMERDLKT

>SGPr567 1 SEQID 104

PAGASPAGASPAGASPARASPALASLSRSSSGRSSSARSASVTTSPTRVYLVRATPVGAVPIRSSPARSAPATRATRE MERDSHGNASPARTPSAGASPAQASPAGTPPGRASPAQASPAQASPAGTPPGRASPAQASPAGAPAGTPPGRASPGRAS SPVQFWQGHTGIRYKEQRESCPKHAVRCDGVVDCKLKSDELGCVRFDWDKSLLKIYSGSSHQWLPICSSNWNDSYS **EKTCOOLGFESAHRTTEVAHRDFANSFSILRYNSTIQESLHRSECPSORYISLOCSHCGLRAMTGRIVGGALASDSKW** >WQVSLHFGTTHICGGTLIDAQWVLTAAHCFFVTREKVLEGWKVYAGTSNLHQLPEAASIAEIIINSNYTDEEDDYDIAL <u> WRLSKPLTLSAHIHPACLPMHGQTFSLNETCWITGFGKTRETDDKTSPFLREVQVNLIDFKKCNDYLVYDSYLTPRMM</u> SAGDLRGGRDSCQGDSGGPLVCEQNNRWYLAGVTSWGTGCGQRNKPGVYTKVTEVLPWIYSKMESEVRFRKS

>SGPr479 1 SEQID 105

HYAGLHVCGGSILNEYWVLSAAHCFHRDKNIKIYDMYVGLVNLRVAGNHTQWYEVNRVILHPTYEMYHPIGGDVALVQ -KTRIVFSESVLPVCLATPEVNLTSANCWATGWGLVSKQGETSDELQEVQLPLILEPWCHLLYGHMSYIMPDMLCAGD <u>MAAPASVĪMGPLGPSĀLGLLLLLLVVAPPRVAALVHRQPENQGISLTGSVACGRPSMEGKILGGVPAPERKWPWQVSV</u> LNAKTVCEGDSGGPLVCEFNRSWLQIGIVSWGRGCSNPLYPGVYASVSYFSKWICDNIEITPTPAQPAPALSPALGPT SVLMAMLAGWSVL

>SGPr489 1 SEQID 106

C G G D S G G S L M C R N K G A W D S G W S I W E A Q V G G S L E S R S S R P S L G N K V R L C L T N N F F K L A G C G T W C S E Q D V I V S G A EGKLHFPESLHLYYESKQRCVWTLLVPEEMHVLLSFSHLDVESCHHSYLSMYSLEDRPIGKFCGESLPSSILIGSNSLR 3DCTSDYVTVHSDVERKKEIARLCGYDVPTPVLSPSSIMLISFHSDENGTCRGFQAIVSFIPKAVYPDLNISISEDESMFL CGGSIVSPQWVITAAHCIANRNIVSTLNVTAGEYDLSQTDPGEQTLTIETVIIHPHFSTKKPMDYDIALLKMAGAFQFGH FVGPICLPELREQFEAGFICTTAGWGRLTEGGVLSQVLQEVNLPILTWEECVAALLTLKRPISGKTFLCTGFPDGGRDA <u>MSLKMLISRNKLILLLGIVFFERGKSATLSLPKAPSCGQSLVKVQPWNYFNIFSRILGGSQVEKGSYPWQVSLKQRQKH</u> KFVSDATDYAAGFNLTYKALKPNYIPGCSYLTVLFEEGLIQSLNYPENYSDKANCDWIFQASKHHLIKLSFQSLEIEES

>SGPr465_1_SEQID_107

IVCGSFFQPQYPGQPSSSDYTIHEDMLCAGDLITGKAICRVNSRGPLVCPLNGTWFLMGLSSWSLDCCSPVGPRVFT HADYNELHRMGSDITLLQLHHHVEFSSHILPACLPEPTTWLAPDSSCWISGWGMVTEDVFLPEPFQLQEAEVGVMDN RWPWQASLLYLGGHICGAALIDSNWVASAAHCFQRCIFPPRAPLSTNPSDYRILLGYDQQSHPTEHSKQMTVNKIMV **RLPYFTNWISQKKRESTPPDPALAPPQETPPALDSMTSQGIVHKPGLCAALLAAHMFLLLLILLGSI**

>SGPr524 1 SEQID 108

MDKENSDVSAAPADLKISNISVQVVSAQKKLPVRRPPLPGRRLPLPGRRPPQRPIGKAKPKKQSKKKVPFWNVQNKIIL <u>EYGSYNISQPCPVGSFRCSSGLCVPQAQRCDGVNDCFDESDELFCVSPQPACNTSSFRQHGPLICDGFRDCENGRD</u> VADVSSNNKGGLLVHFWIVFVMPRAKGHIFCEDCVAAILKDSIQTSIINRTSVGSLQGLAVDMDSVVLNGDCWSFLKK KRRENGAVSTDKGCSQYFYAEHLSLHYPLEISAASGRLMCHFKLVAIVGYLIRLSIKSIQIEADNCVTDSLTIYDSLLPIR /GSAYCGASVISREWLLSAAHCFHGNRLSDPTPWTAHLGMYVQGNAKFVSPVRRIVVHEYYNSQTFDYDIALLQLSIA CTWKFQTSLSTLGIALKFYNYSITKKSMKGCEHGWWEINEHMYCGSYMDHQTIFRVPSPLVHIQLQCSSRLSDKPLLA SSILYRICEPTRTLMSFVSTNNLMLVTFKSPHIRRLSGIRAYFEVIPEQKCENTVLVKDITGFEGKISSPYYPSYYPPKCK EQNCTQSIPCNNRTFKCGNDICFRKQNAKCDGTVDCPDGSDEEGCTCSRSSSALHRIIGGTDTLEGGWPWQVSLHF NPETLKQLIQPICIPPTGQRVRSGEKCWVTGWGRRHEADNKGSLVLQQAEVELIDQTLCVSTYGIITSRMLCAGIMSG **-TVFLFILAVIAWTLLWLYISKTESKDAFYFAGMFRITNIEFLPEYRQKESREFLSVSRTVQQVINLVYTTSAFSKFYEQS** KRDACKGDSGGPLSCRRKSDGKWILTGIVSWGHGCGRPNFPGVYTRVSNFVPWIHKYVPSL

>SGPr422 SEQID 109

DDIRQICLPEASASFQPNLTVHITGFGALYYGGESQNDLREARVKIISDDVCKQPQVYGNDIKPGMFCAGYMEGIYDAC MTLNKIKDLFAGKGQWDLAPEAEMLKPWMIAVLIVLSLTVVAVTIGLLVHFLVFDQKKEYYHGSFKILDPQINNNFGQSN DNIHQCGATLISNTWLVTAAHCFQKYKNPHQWTVSFGTKINPPLMKRNVRRFIIHEKYRSAAREYDIAVVQVSSRVTFS NVAMVKNGNVGPGSGAGEAPGLGAGPAWSPMSSSTGELTVQASCGKRVVPLNVNRIASGVIAPKAAWPWQASLQY RGDSGGPLVTRDLKDTWYLIGIVSWGDNCGQKDKPGVYTQVTYYRNWIASKTGI

>SGPr538_SEQID_110

YDVALLRLQTALNFSDTVGAVCLPAKEQHFPKGSRCWVSGWGHTHPSHTYSSDMLQDTVVPLFSTQLCNSSCVYSG **WQASVALGFRHTCGGSVLAPRWVVTAAHCMHSFRLARLSSWRVHAGLVSHSAVRPHQGALVERIIPHPLYSAQNHD** ASQPISGTLQDEEITLSCSEASAEEALLPALPKTVSFRINSEDFLLEAQVRDQPRWLLVCHEGWSPALGLQICWSLGHL RLTHHKGVNLTDIKLNSSQEFAQLSPRLGGFLEEAWQPRNNCTSGQVVSLRCSECGARPLASRIVGGQSVAPGRWP MSLMLDDQPPMEAQYAEEGPGPGIFRAEPGDQQHPISQAVCWRSMRRGCAVLGALGLLAGAGVGSWLLVLYLCPA ALTPRMLCAGYLDGRADACQGDSGGPLVCPDGDTWRLVGVVSWGRACAEPNHPGVYAKVAEFLDWIHDTAQDSL

>SGPr527 1 SEQID 111

YLGRAGASSLPQGHQVSRLVISIRLPQHLGLRPPLALLELSSRVEPSPSALPICLHPAGIPPGASCWVLGWKEPQDRVP <u>MARHLLLPLVMLVISPIPGAFQDSALSPTQEEPEDLDCGRPEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIA</u> **VAAAVSILTQRICDCLYQGILPPGTLCVLYAEGQENRCEMTSAPPLLCQMTEGSWILVGMAVQGSRELFAAIGPEEAWI** *N*PVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQCLYSQPGPFNLTLQILPGMLCAGY QSDPQEPREENCTIALPECGKAPRPGAWPWEAQVMVPGSRPCHGALVSESWVLAPASCFLDPNSSDSPPRDLDAW PEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYEAWIREQVMGSEPGPAFPTQPQKT PGALLEAELLGGWWCHCLYGRQGAAVPLPGDPPHALCPAYQEKEEVGSCWTHGPWISHVTRGAYLEDQLAWDWG PDGEETETQTCPPHTEHGACGLRLEAAPVGVLWPWLAEVHVAGDRVCTGILLAPGWVLAATHCVLRPGSTTVPYIEV 28WVLSAAHCFMTNGTLEPAAEWSVLLGVHSQDGPLDGAHTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAV RVLLPSRPRAERVARLVQHENASWDNASDLALLQLRTPVNLSAASRPVCLPHPEHYFLPGSRCRLARWGRGEPALG SQTVGEANFLPPSGSPHWPTGGSNLCPPELAKASGSPHAVYFLLLTTLLIQS

SGPr542_SEQID_112

4GTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPDVCNSSWKGHLTLTMLCTRSGDSHRRGFCSADSGGPLVCRNR **CFSHRDLRTGLVVLGAHVLSTAEPTQQVFGIDALTTHPDYHPMTHANDICLLQLNGSAVLGPAVGLLRLPGRRARPPT** AMGLGLRGWGRPLLTVATALMLPVKPPAGSWGAQIIGGHEVTPHSRPYMASVRFGGQHHCGGFLLRARWVVSAAH AHGLVSFSGLWCGDPKTPDVYTQVSAFVAWIWDVVRRSSPQPGPLPGTTRPPGEAA

>SGPr551 SEQID 113

MLSPEVVQALLVEELLSTVNSSAAVPYRAEYEVDPEGLVILEASVKDIAALNSTLGCYRYSYVGQGQVLRLKGPDHLAS DPFVLSVQPVVFQACEVNLTLDNRLDSQGVLSTPYFPSYYSPQTHCSWHLTVPSLDYGLALWFDAYALRRQKYDLPC TQGQWTIQNRRLCGLRILQPYAERIPVVATAGITINFTSQISLTGPGVRVHYGLYNQSDPCPGEFLCSVNGLCVPACDG MPVAEAPQVAGGGGGGGGGGEEAEPEGMFKACEDSKRKARGYLRLVPLFVLLALLVLASAGVLLWYFLGYKAEVMVS SCLWHLQGPKDLMLKLRLEWTLAECRDRLAMYDVAGPLEKRLITSVYGCSRQEPVVEVLASGAIMAVVWKKGLHSYY MITGWGALREGGPISNALQKVDVQLIPQDLCSEAYRYQVTPRMLCAGYRKGKKDACQGDSGGPLVCKALSGRWFLA QVYSGSLRVLNRHFSQDLTRRESSAFRSETAKAQKMLKELITSTRLGTYYNSSSVYSFGEGPLTCFFWFILQIPEHRRL **JGRPDCRDGSDEEHCDCGLQGPSSRIVGGAVSSEGEWPWQASLQVRGRHICGGALIADRWVITAAHCFQEDSMAS** /KDCPNGLDERNCVCRATFQCKEDSTCISLPKVCDGQPDCLNGSDEEQCQEGVPCGTFTFQCEDRSCVKKPNPQC VLWTVFLGKVWQNSRWPGEVSFKVSRLLLHPYHEEDSHDYDVALLQLDHPVVRSAAVRPVCLPARSHFFEPGLHC 3LVSWGLGCGRPNYFGVYTRITGVISWIQQVVT OPENSOLD COLOCI

>SGPr451 SEQID 114

TAPLKDVLQGSRIIGGTEAQAGAWPWVVSLQIKYGRVLVHVCGGTLVRERWVLTAAHCTKDTSDPLMWTAVIGTNNIH AEVHYISREMCNSERSYGGIIPNTSFCAGDEDGAFDTCRGDSGGPLMCYLPEYKRFFVMGITSYGHGCGRRGFPGVY DLPPSCSPASKMRLGLLSVALLFVGSSHLYSDHYSPSGRHRLGPSPEPAASSQQAEAVRKRLRRRREGGAHAKDCG GRYPHTKKIKIKAIIIHPNFILESYVNDIALFHLKKAVRYNDYIQPICLPFDVFQILDGNTKCFISGWGRTKEEGNATNILQD **GPSFYQKWLTEHFFHASTQGILTINILRGQILIALCFVILLATT**

>SGPr452_1_SEQID_115

GHNAPPGKWPWQVSLRVYSYHWASWAHICGGSLIHPQWVLTAAHCIFWKDTDPSIYRIHAGDVYLYGGRGLLNVSRI SPPQPRTPDCRLQASLEALATLAPQPSDWLCFADLGWFEADGAAHSMGLGSSLKWAWAKPSGMPVPENDLVGIVG IVHPNYVTAGLGADVALLQLPGSPLSPESLPPPYRLQQASVQVLENAVCEQPYRNASGHTGDRQLILDDMLCAGSEG RDSCYGDSGGPLVCRLRGSWRLVGVVSWGYGCTLRDFPGVYTHVQIYVLWILQQVGELP

>SGPr504_SEQID_116 IIGGHEVTPHSRPYMASVRFGGQHHCGGFLLRARWVVSAAQCFSH >SGPr469_SEQID_117 GDSGGPLVCELNGTWVQVGIVSWGIGCGRKGYPGVYTEVSFYKKWI

HVCSDTLISEEWVLTVAICFPLSPHPDFQANTSSAIAVVELPSPVSVSPVVLLICLPSSEVYLKKNTTSCWVTGWGYTGI _KSGPFRIWQGVKTKGEEGDRDTGTAGYAFTLLLLLGISGEPPEWVCGRPTVSSGIASGLGASVGQWPWQVSIRQGL MAGEQVTANVSRYPGQKTMSFPEKTFLLSYRASLLAVVTHRSNNSRGRAFESQVLPDLTAGDAADPPIPPLGPGAAL "QYIKRSYTLKELKVPLIDLQTCGDHYQNEILLHGVELIISEAMICSKLPVGQMDQCTVRIHPSGTFHRPCLPQ >SGPr400_SEQID_118